

	Type	L #	Hits	Search Text	DBs	Time Stamp	Complaints	Comments or Errors on Definition
1	BRS	L1	109	integrin adj binding adj (motif or domain)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/01/29 08:24		0
2	BRS	L2	3405	rgd	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/01/29 08:24		0
3	BRS	L3	8888	bone adj (growth or formation)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/01/29 08:25		0
4	BRS	L4	32	(1 or 2) same 3	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/01/29 08:51		0
5	BRS	L5	2	wo-9514714-\$ did.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/01/29 08:26		0
6	BRS	L6	2	5681353.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/01/29 08:51		0

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Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	15	10 US-09-812-485A-47	Sequence 47, Appli
2	82	100.0	15	12 US-10-360-202-10	Sequence 1, Appli
3	82	100.0	19	12 US-10-360-202-9	Sequence 7, Appli
4	82	100.0	19	12 US-10-360-202-9	Sequence 9, Appli
5	82	100.0	20	12 US-10-360-202-8	Sequence 8, Appli
6	82	100.0	21	12 US-10-360-202-6	Sequence 6, Appli
7	82	100.0	23	10 US-09-812-485A-49	Sequence 49, Appli
8	82	100.0	23	12 US-10-360-202-1	Sequence 17, Appli
9	82	100.0	24	12 US-10-360-202-17	Sequence 18, Appli
10	82	100.0	24	12 US-10-360-202-18	Sequence 1, Appli
11	82	100.0	97	10 US-09-812-485A-1	Sequence 1, Appli
12	82	100.0	509	12 US-09-794-422-34	Sequence 34, Appli
13	82	100.0	525	10 US-09-814-550-2	Sequence 2, Appli
14	82	100.0	525	12 US-09-794-422-6	Sequence 6, Appli
15	82	100.0	525	12 US-10-311-840-1	Sequence 1, Appli

Sequence 10, Application US/10360202  
*i* Publication No. US20030186891A1  
*i* GENERAL INFORMATION:  
*i*   APPLICANT: Okano, Toshio  
*i*   APPLICANT: Tsugawa, Naoko  
*i*   APPLICANT: Nakagawa, Kimie  
*i*   APPLICANT: Blacher, Russell W  
*i*   APPLICANT: Kumagai, Yoshihori  
*i*   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
*i*   TITLE OF INVENTION: OF VITAMIN D DEFICIENCY  
*i*   FILE REFERENCE: BEAR-010  
*i*   CURRENT APPLICATION NUMBER: US/10/360,202  
*i*   CURRENT FILING DATE: 2003-02-07  
*i*   PRIOR APPLICATION NUMBER: 60/335,548  
*i*   PRIOR FILING DATE: 2002-02-08  
*i*   NUMBER OF SEQ ID NOS: 23  
*i*   SOFTWARE: FastSEQ for Windows Version 4.0  
*i*   SEQ ID NO: 10  
*i*   LENGTH: 15  
*i*   TYPE: PRT  
*i*   ORGANISM: Artificial sequence  
*i*   FEATURE:  
*i*   ; OTHER INFORMATION: Synthetic oligopeptide  
*US-10-360-202-9*

Query Match   100.0%; Score 82; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ERGDDNDISPFSGDGQ 15  
Db   1 ERGDDNDISPFSGDGQ 15

RESULT 5  
*US-10-360-202-8*  
*i* Sequence 8, Application US/10360202  
*i* Publication No. US20030186891A1  
*i* GENERAL INFORMATION:  
*i*   APPLICANT: Okano, Toshio  
*i*   APPLICANT: Tsugawa, Naoko  
*i*   APPLICANT: Nakagawa, Kimie  
*i*   APPLICANT: Blacher, Russell W  
*i*   APPLICANT: Kumagai, Yoshihori  
*i*   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
*i*   TITLE OF INVENTION: OF VITAMIN D DEFICIENCY  
*i*   FILE REFERENCE: BEAR-010  
*i*   CURRENT APPLICATION NUMBER: US/10/360,202  
*i*   CURRENT FILING DATE: 2003-02-07  
*i*   PRIOR APPLICATION NUMBER: 60/335,548  
*i*   PRIOR FILING DATE: 2002-02-08  
*i*   NUMBER OF SEQ ID NOS: 23  
*i*   SOFTWARE: FastSEQ for Windows Version 4.0  
*i*   SEQ ID NO: 9  
*i*   LENGTH: 19  
*i*   TYPE: PRT  
*i*   ORGANISM: Artificial sequence  
*i*   FEATURE:  
*i*   ; OTHER INFORMATION: Synthetic oligopeptide  
*US-10-360-202-8*

Query Match   100.0%; Score 82; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ERGDDNDISPFSGDGQ 15  
Db   1 ERGDDNDISPFSGDGQ 15

RESULT 6  
*US-10-360-202-6*  
*i* Sequence 6, Application US/10360202  
*i* Publication No. US20030186891A1

RESULT 4  
*US-10-360-202-9*  
*i* Sequence 9, Application US/10360202

GENERAL INFORMATION:  
 ; APPLICANT: Okano, Toshio  
 ; APPLICANT: Tsugawa, Naoko  
 ; APPLICANT: Nakagawa, Kimie  
 ; APPLICANT: Blacher, Russell W  
 ; APPLICANT: Kumagai, Yoshihori  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
 ; FILE REFERENCE: BEAR-010  
 ; CURRENT APPLICATION NUMBER: US/10/360,202  
 ; CURRENT FILING DATE: 2003-02-07  
 ; PRIORITY NUMBER: 60/335,548  
 ; PRIOR FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 6  
 LENGTH: 21  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligopeptide  
 US-10-360-202-6

Query Match Similarity 100.0%; Score 82; DB 12; Length 23;  
 Best Local Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPFSGDQ 15  
 Db 5 ERGDNDISPFSGDQ 19

RESULT 7  
 US-09-812-485A-49  
 Sequence 49, Application US/09812485A  
 Publication No. US20020197267A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Kumagai, Yoshihori  
 ; APPLICANT: Blacher, Russell W  
 ; APPLICANT: Yoneda, Toshiyuki  
 ; TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases  
 ; FILE REFERENCE: BEAR-006CIP  
 ; CURRENT APPLICATION NUMBER: US/09/812,485A  
 ; CURRENT FILING DATE: 2001-03-19  
 ; PRIOR FILING DATE: 2000-08-16  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 49  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: D-00006 peptide  
 NAME/KEY AMIDATION LOCATION: 15

US-09-812-485A-49

Query Match Similarity 100.0%; Score 82; DB 10; Length 23;  
 Best Local Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPFSGDQ 15  
 Db 5 ERGDNDISPFSGDQ 19

RESULT 8  
 US-10-160-202-11  
 Sequence 11, Application US/10360202  
 Publication No. US20030186891A1  
 GENERAL INFORMATION:

APPLICANT: Okano, Toshio  
 ; APPLICANT: Tsugawa, Naoko  
 ; APPLICANT: Nakagawa, Kimie  
 ; APPLICANT: Blacher, Russell W  
 ; APPLICANT: Kumagai, Yoshihori  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
 ; TITLE OF INVENTION: OF VITAMIN D DEFICIENCY  
 ; FILE REFERENCE: BEAR-010  
 ; CURRENT APPLICATION NUMBER: US/10/360,202  
 ; CURRENT FILING DATE: 2003-02-07  
 ; PRIORITY NUMBER: 60/335,548  
 ; PRIOR FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligopeptide  
 US-10-360-202-1

Query Match Similarity 100.0%; Score 82; DB 12; Length 23;  
 Best Local Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPFSGDQ 15  
 Db 5 ERGDNDISPFSGDQ 19

RESULT 9  
 US-10-360-202-17  
 Sequence 17, Application US/10360202  
 Publication No. US20030186891A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Okano, Toshio  
 ; APPLICANT: Tsugawa, Naoko  
 ; APPLICANT: Nakagawa, Kimie  
 ; APPLICANT: Blacher, Russell W  
 ; APPLICANT: Kumagai, Yoshihori  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
 ; TITLE OF INVENTION: OF VITAMIN D DEFICIENCY  
 ; FILE REFERENCE: BEAR-010  
 ; CURRENT APPLICATION NUMBER: US/10/360,202  
 ; CURRENT FILING DATE: 2003-02-07  
 ; PRIORITY NUMBER: 60/335,548  
 ; PRIOR FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 17  
 LENGTH: 24  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic oligopeptide  
 US-10-360-202-17

Query Match Similarity 100.0%; Score 82; DB 12; Length 24;  
 Best Local Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPFSGDQ 15  
 Db 6 ERGDNDISPFSGDQ 20

RESULT 10  
 US-10-160-202-18  
 Sequence 18, Application US/10360202  
 Publication No. US20030186891A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Okano, Toshio

APPLICANT: Tsugawa, Naoko  
; APPLICANT: Nakagawa, Kimie  
; APPLICANT: Blacher, Russell W  
; TITLE OF INVENTION: Kumagai, Yoshinari  
; COMPOSITIONS AND METHODS FOR TREATMENT  
; FILE REFERENCE: BEAR-010  
; CURRENT FILING DATE: 2003-02-07  
; PRIORITY APPLICATION NUMBER: US/10/360,202  
; PRIORITY FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1.8  
; LENGTH: 24  
; TYPE: PRF  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligopeptide  
; US-10-360-202-18

Query Match 100.0%; Score 82; DB 12; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPGDGQ 15  
Db 5 ERGDNDISPGDGQ 19

RESULT 11  
US-09-812-485A-1  
Sequence 1. Application US/09812485A  
Publication No. US20020197267A1.  
GENERAL INFORMATION:  
APPLICANT: Kumagai, Yoshinari  
APPLICANT: Blacher, Russell W  
APPLICANT: Yoneda, Toshiyuki  
TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases  
FILE REFERENCE: BEAR-006CIP  
CURRENT APPLICATION NUMBER: US/09/812,485A  
CURRENT FILING DATE: 2001-03-19  
PRIORITY APPLICATION NUMBER: 09/641,034  
PRIORITY FILING DATE: 2000-08-16  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 1  
LENGTH: 97  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptidic compound

Query Match 100.0%; Score 82; DB 10; Length 97;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPGDGQ 15  
Db 47 ERGDNDISPGDGQ 61

RESULT 12  
US-09-794-422-34  
Sequence 34. Application US/09794422  
Publication No. US20030166239AA1  
GENERAL INFORMATION:  
APPLICANT: Brown, Thomas A.  
APPLICANT: De Wet, Jeffrey R.  
APPLICANT: Gowen, Lori C.  
APPLICANT: Hames, Lynn M.  
TITLE OF INVENTION: Mammalian Osteoregulins  
FILE REFERENCE: PC10445  
CURRENT APPLICATION NUMBER: US/09/794,422  
CURRENT FILING DATE: 2001-02-27

; TITLE OF INVENTION: Mammalian Osteoregulins  
; FILE REFERENCE: PC10445  
; CURRENT APPLICATION NUMBER: US/09/794,422  
; CURRENT FILING DATE: 2001-02-27  
; PRIORITY APPLICATION NUMBER: 60/185,617  
; PRIORITY FILING DATE: 2000-02-29  
; PRIORITY APPLICATION NUMBER: 60/234,500  
; PRIORITY FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 34  
; LENGTH: 509  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-794-422-34

Query Match 100.0%; Score 82; DB 12; Length 509;  
Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPGDGQ 15  
Db 230 ERGDNDISPGDGQ 244

RESULT 13  
US-09-814-550-2  
Sequence 2. Application US/09814550  
Patent No. US2010102641A1  
GENERAL INFORMATION:  
APPLICANT: Schiavi, Susan  
APPLICANT: Madden, Stephen  
APPLICANT: Manavalan, Parthasarathy  
APPLICANT: Levine, Michael  
APPLICANT: Jan de Beur, Suzanne  
TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1  
FILE REFERENCE: 50144US  
CURRENT FILING DATE: 2001-03-22  
PRIORITY APPLICATION NUMBER: US 60/191,786  
PRIORITY FILING DATE: 2000-03-24  
PRIORITY APPLICATION NUMBER: US 60/241,598  
PRIORITY FILING DATE: 2000-10-19  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO: 2  
LENGTH: 525  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-814-550-2

Query Match 100.0%; Score 82; DB 10; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPGDGQ 15  
Db 246 ERGDNDISPGDGQ 260

RESULT 14  
US-09-794-422-6  
Sequence 6. Application US/09794422  
Publication No. US20030166239A1  
GENERAL INFORMATION:  
APPLICANT: Brown, Thomas A.  
APPLICANT: De Wet, Jeffrey R.  
APPLICANT: Gowen, Lori C.  
APPLICANT: Hames, Lynn M.  
TITLE OF INVENTION: Mammalian Osteoregulins  
FILE REFERENCE: PC10445  
CURRENT APPLICATION NUMBER: US/09/794,422  
CURRENT FILING DATE: 2001-02-27

```

; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-794-422-6

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Query Match          100.0%;  Score 82;  DB 12;  Length 525;
Best Local Similarity 100.0%;  Pred. No. 2.4e-05;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ERGDNDISPGDGQ 15
Db      246 ERGDNDISPGDGQ 260

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RESULT 15

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US-10-311-840-1
; Sequence 1, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, TakaO
; TITLE OF INVENTION: No. US20030175808A1 el Protein and its DNA
; FILE REFERENCE: 2734USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Human
; US-10-311-840-1

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Query Match          100.0%;  Score 82;  DB 12;  Length 525;
Best Local Similarity 100.0%;  Pred. No. 2.4e-05;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ERGDNDISPGDGQ 15
Db      246 ERGDNDISPGDGQ 260

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Search completed: January 29, 2004, 12:42:43  
Job time : 21.3158 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	30	39	47.6	402	1	F48552
OM protein - protein search, using sw model	31	39	47.6	416	2	C39200	
Run on: January 29, 2004, 12:36:28 ; Search time 10:6579 Seconds	32	39	47.6	507	2	G89908	
(without alignments)	33	39	47.6	535	2	T29430	
135.349 Million cell updates/sec	34	39	47.6	564	2	D96017	
Title: US-09-812-485A-47	35	39	47.6	576	1	A5049	
Perfect score: 82	36	39	47.6	612	2	S65196	
Sequence: 1 ERGDDNDISPFSGDQ 15	37	39	47.6	792	2	F71894	
Scoring table: BLOSUM62	38	39	47.6	1166	2	S37692	
Gapop 10.0 , Gapext 0.5	39	39	47.6	1526	2	DNA topoisomerase	
Searched: 283308 seqs, 96168682 residues	40	39	47.6	1528	2	DNA topoisomerase	
Total number of hits satisfying chosen parameters:	283308						
Minimum DB seq length: 0							
Maximum DB seq length: 2000000000							
Post-processing: Minimum Match 0% ; Maximum Match 100%							
Database : PIR_76:*							
1: pir1:*							
2: pir2:*							
3: pir3:*							
4: pir4:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	45	54.9	913	2 DB82885	multiple banded an		
2	44	53.7	277	2 D73322	lysozyme (EC 3.2.1.2.1		
3	43	52.4	444	2 B83891	intracellular alka		
4	43	52.4	629	2 T31285	probable transmembr		
5	43	52.4	1758	2 F88559	protein C48B4.4b [		
6	43	52.4	1767	2 S60124	transport protein		
7	42	51.2	420	2 AE1857	hypothetical prote		
8	42	51.2	874	2 AD3322	leucyl-tRNA synthet		
9	42	51.2	1209	2 T11537	brahma associated		
10	41	50.0	337	2 S38166	hypothetical prote		
11	41	50.0	886	2 G65036	hypothetical prote		
12	41	50.0	1166	2 S33812	myosin-like protei		
13	40	48.8	140	2 GB4608	Bn/Spm-like transp		
14	40	48.8	237	2 AF0724	probable exported		
15	40	48.8	300	2 F90274	hypothetical prote		
16	40	48.8	304	2 FB3642	probable transcript		
17	40	48.8	357	2 CB4856	probable protein k		
18	40	48.8	381	2 BB7470	hypothetical prote		
19	40	48.8	393	2 SS5499	cellulase egII - B		
20	40	48.8	464	2 B35159	arylsulfatase [EC		
21	40	48.8	577	2 T45548	hypothetical prote		
22	40	48.8	798	2 T31022	protein F10G7.2 [i		
23	40	48.8	914	2 B88131	unknown protein [i		
24	39	47.6	156	2 B90562	2-keto-4-pentenoat		
25	39	47.6	269	2 E90679	probable hydratase		
26	39	47.6	269	2 A8530	dihydrodipicolinat		
27	39	47.6	271	2 F63762	S-adenosylmethiononi		
28	39	47.6	300	2 H70879			
29	39	47.6	347	2 A83170			
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					Alignments		

Best Local Similarity 66.7%; Pred. No.: 10; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RGNDISPPSGD 13  
Db 252 RGDDADINTFAGD 263

RESULT 3

B8891 intracellular alkaline serine proteinase aprx [imported] - *Bacillus halodurans* (strain Q) C;Species: *Bacillus halodurans*  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C;Accession: B8891  
R;Takami, H.; Nakagone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and A;Reference number: A83650; MUID:20512582; PMID:11056132  
A;Accession: B8891  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-444 <STO>  
A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BA005649.1; GSPDB:GN000004  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: aprX

Query Match Score 43; DB 2; Length 444;  
Best Local Similarity 50.0%; Pred. No.: 25; Matches 3; Indels 0; Gaps 0;

Qy 1 ERGNDISPFSGDG 14  
Db 322 DREDDDVAPPSSRG 335

RESULT 4

T3285 probable transmembrane protein - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jun-2000  
C;Accession: T39285  
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Bothe, G.; Pohl, T.  
submitted to the EMBL Data Library, July 1999  
A;Reference number: Z22841  
A;Accession: T39285  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-629 <MCD>  
A;Cross-references: EMBL:AL096851; PIDN:CA850971.1; GSPDB:GN00067; SPBCL1105.08  
A;Experimental source: strain 972h-; cosmid c1105  
C;Genetics:  
A;Gene: SPDB:SPBCL1105.08  
A;Map position: 2  
A;Introns: 67/1  
C;Superfamily: *Schizosaccharomyces pombe* probable transmembrane protein SPBCL1105.08

Query Match Score 43; DB 2; Length 629;  
Best Local Similarity 72.7%; Pred. No.: 37; Matches 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 NDISPFGDG 15  
Db 48 NTISSPFIGGGR 58

RESULT 5

F88559 protein C48B4.4b [imported] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 17-May-2002  
C;Accession: F88555  
R;anonymous, The *C. elegans* Sequencing Consortium.

Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
A;Reference number: A75000; MUID:9909613; PMID:9851916  
A;Note: see websites Genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: F88559  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1758 <STO>  
A;Cross-references: GB:chr\_III; PIDN:CAA82384.1; PID:93875025; GSPDB:GN00021; CESP:C48B4  
C;Genetics:  
A;Gene: C48B4.4b  
A;Map Position: 3  
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
Query Match Score 43; DB 2; Length 1758;  
Best Local Similarity 53.3%; Pred. No.: 1.1e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 ERGNDISPFSGDG 15  
Db 42 ENESNDSTPLRGDGQ 56

RESULT 6

S60124 transport protein homolog C48B4.4 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Accession: S60124; S40724; S40725  
R;Kershaw, J.  
submitted to the EMBL Data Library, November 1995  
A;Reference number: S60124  
A;Accession: S60124  
A;Molecule type: DNA  
A;Residues: 1-1767 <KER>  
A;Cross-references: EMBL:229117; PID:9439247; PID:g1066912  
C;Genetics:  
A;Map Position: III  
A;Introns: 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/1;  
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
C;Keywords: ATP; duplication; nucleotide binding; P-loop; transmembrane protein  
F1628-818/Domain: ATP-binding cassette homology <ABC1>  
F1645-652/Region: nucleotide-binding motif A (P-loop)  
F164-769/Region: nucleotide-binding motif B  
F1457-1642/Region: ATP-binding cassette homology <ABC2>  
F1474-1481/Region: nucleotide-binding motif A (P-loop)  
F1586-1591/Region: nucleotide-binding motif B

Query Match Score 43; DB 2; Length 1767;  
Best Local Similarity 53.3%; Pred. No.: 1.1e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ERGNDISPFSGDG 15  
Db 42 ENESNDSTPLRGDGQ 56

RESULT 7

AEI857 hypothetical protein al10406 [imported] - *Nostoc* sp. (strain PCC 7120)  
C;Species: *Nostoc* sp. PCC 7120  
A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C;Accession: AEI857  
R;Kaneo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.; Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-13, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Status: preliminary  
A;Molecule type: DNA

A:Residues: 1-420 <KDR>  
 A:Cross-references: GB:BA000019; PIDN:BAB72364.1; PID:g17129751; GSPDB:GN00179  
 A:Experimental source: strain pCC 7120  
 C:Genetics:  
 A:Gene: all0406

Db      |||||: | | | | : | | | |  
 380 RGDNMPPIKG 390

## RESULT 10

S38166 hypothetical protein YKR088C - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: hypothetical protein YKR408  
 C:Species: *Saccharomyces cerevisiae*  
 C:Accession: S38166; S42017; S39129  
 R:Baladron, V.; Balibesta, J.P.G.; Bou, G.; del Rey, P.; Esteban, P.F.; Garcia-Cantalejo, A;Submitted to the Protein Sequence Database, March 1994  
 A:Reference number: S38158  
 A:Accession: S38166  
 A:Molecule type: DNA  
 A:Residues: 1-337 <BAL>  
 A:Cross-references: ENBL:Z28313; NID:9486572; PIDN:CRA82167.1; PID:g486573; MIPS:YKR088C  
 A:Experimental source: strain S288C  
 R:Garcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santos, M.A.; Bou, G.; Remacha, M.A.  
 Yeast 10., 231-245, 1994  
 A:Title: The complete sequence of an 18,002 bp segment of *Saccharomyces cerevisiae* chromosome  
 A:Accession: S42017  
 A:Map position: 1-337 <GAR>  
 A:Molecule type: DNA  
 A:Cross-references: ENBL:227116; NID:9415899; PIDN:CAA81639.1; PID:g415908  
 A:Experimental source: strain S288C  
 C:Genetics:  
 A:Map position: 11R  
 A:Cross-references: SGD:S0001796  
 C:Keywords: transmembrane protein  
 F:96-112/Domain: transmembrane #status predicted <TM1>  
 F:138-154/Domain: transmembrane #status predicted <TM2>  
 F:174-190/Domain: transmembrane #status predicted <TM3>  
 F:290-306/Domain: transmembrane #status predicted <TM4>

Query Match Score 42; DB 2; Length 420;  
 Best Local Similarity 51.2%; Pred. No. 35; Indels 1; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 1; .Indels 0; Gaps 0;  
 Qy 5 NDISPFSGDG 14  
 Db 60 NGINPFAAGG 69

Db      |||||: | | | | : | | | |  
 380 RGDNMPPIKG 390

## RESULT 8

D75307 leucyl-tRNA synthetase - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
 C:Accession: D75307  
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Ventevor, J.C.; Fraser, C.M.; Science 286, 1571-1577, 1999  
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
 A:Reference number: A75250; MUID:20036896; PMID:10567266  
 A:Accession: D75307  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-874 <WHI>  
 A:Cross-references: GB:AE002050; GB:AE000513; NID:g6459965; PIDN:AAF11720.1; PID:g645997  
 A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR2174  
 A:Map position: 1  
 C:Superfamily: leucine-tRNA ligase

Query Match Score 42; DB 2; Length 874;  
 Best Local Similarity 51.2%; Pred. No. 77; Indels 4; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 4; .Indels 0; Gaps 0;  
 Qy 3 GDNDISPFSGDGQ 15  
 Db 430 GDQPSEPFGEGQ 442

Db      |||||: | | | | : | | | |  
 380 RGDNMPPIKG 390

## RESULT 11

G65036 hypothetical protein b2584 - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C:Accession: G65036  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coli Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of *Escherichia coli* K-12.  
 A:Reference number: A64720; MUID:9726617; PMID:9278503  
 A:Accession: G65036  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-886 <BLAT>  
 A:Cross-references: GB:AE000344; GB:U00096; NID:g1788927; PIDN:AACT5637.1; PID:g1788938;  
 A:Experimental source: strain K-12, substrain MG1655

Query Match Score 41; DB 2; Length 886;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;  
 Matches 7; Conservative 1; Mismatches 2; .Indels 0; Gaps 0;  
 Qy 6 DISPFSGDQ 15  
 Db 693 DISPEFGDNE 702

Db      |||||: | | | | : | | | |  
 380 RGDNMPPIKG 390

## RESULT 12

A:Accession: AF0772

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 &lt;PAR&gt;

A:Cross-references: GB:AL513382; PIDN:CAD02500\_1; PID:916503364; GSPDB:GN00176

C:Accession: S33812

R:Knight, A.E.; Kendrick-Jones, J.

J. Mol. Biol. 231, 148-154, 1993

A:Title: A myosin-like protein from a higher plant

A:Reference number: S33812; MUID:93267647; PMID:7684453

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Cross-references: ENB:X69505; NID:9297068; PIDN:CA61875\_1; PID:96491702

C:Superfamily: myosin heavy chain 95F; myosin motor domain homology

C:Keywords: calmodulin binding; coiled coil; nucleotide binding; P-loop

F:256-263/Region: nucleotide-binding motif A (P-loop)

Query Match 50.0% Score 41; DB 2; Length 1166;  
Best Local Similarity 58.3%; Pred. No. 1.5e+02; Indels 0; Gaps 0;  
Matches 7; Conservative 3; Mismatches 2;Qy 3 GDNIDISPPSGDG 14  
Db 63 GDSGDSPPSGHG 74

RESULT 13

En.Spm-like transposon protein [imported] - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Accession: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Date: 02-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001

C:Cross-references: F90274; R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V-Jong, T.; Jeffries, A.C.; Koza, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; submitted to Genbank, April 2001

A:Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A99139

A:Accession: F90274

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-300 &lt;KDR&gt;

A:Cross-references: GB:AE006641; NID:913814401; PIDN:AAK41453\_1; GSPDB:GN00155

A:Gene: porB-1

C:Superfamily: pyruvate synthase beta chain

Query Match 48.8% Score 40; DB 2; Length 300;  
Best Local Similarity 53.3%; Pred. No. 53; Indels 8; Conservative 4; Mismatches 1;Qy 2 RGDNDD--ISPFGDG 14  
Db 90 RGDNDDAVAWAGDG 104

Search completed: January 29, 2004, 12:40:56

Job time : 11.6579 secs

## RESULT 14

AF0772

probable exported protein STY2350 [imported] - *Salmonella enterica* subsp. *enterica* serovar *typhi*C:Species: *Salmonella enterica* subsp. *enterica* serovar *typhi*A:Note: this species has also been called *Salmonella typhi*

C:Accession: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Accession: AF0772

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, Th.T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608



Query Match 51.2%; Score 42; DB 1; Length 823;  
 Best Local Similarity 53.8%; Pred. No. 25; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 4;

Qy 3 DNDISPFSGDQ 15  
 Db 399 GQPSEPYSGEQ 391

RESULT 2

YK68 YEAST STANDARD; PRT; 337 AA.

ID YK68 YEAST  
 AC P36164;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DE Hypothetical 38.3 kDa protein in PRP16-SRP40 intergenic region.  
 GN YKR088C OR YKR408

OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomyctales; Saccharomyctaceae; Saccharomyces.  
 NCBI\_TaxID=4932;

RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:94622327; PubMed:8203164;  
 RA Garcia-Cantalejo J.; Baladron V.; Esteban P.F.; Santos M.A.; Bou G.;  
 RA Remacha M.A.; Revuelta J.L.; Ballesta J.P.G.; Jimenez A.; del Rey F.;  
 RT "The complete sequence of an 18,000 bp segment of Saccharomyces  
 cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 genes,  
 and six new open reading frames.";  
 RT Year 10:231-245 (1994).  
 RL !- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC

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DR EMBL; Z27116; CAA81639\_1; -;  
 DR EMBL; Z28313; CAA8167\_1; -;  
 DR PIR; S38166; S38166.  
 DR SGD; S0001796; YKR088C.

KW Hypothetical protein; Transmembrane.

FT TRANSMEM 96 115 POTENTIAL.  
 FT TRANSMEM 138 162 POTENTIAL.  
 FT TRANSMEM 173 191 POTENTIAL.  
 FT TRANSMEM 222 246 POTENTIAL.  
 FT TRANSMEM 253 271 POTENTIAL.  
 FT TRANSMEM 287 309 POTENTIAL.  
 SQ SEQUENCE 337 AA; 38311 MN; 7EA95DD4E5AFA77FE CRC64;

Query Match 50.0%; Score 41; DB 1; Length 337;  
 Best Local Similarity 65.7%; Pred. No. 14; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 3;

Qy 4 DNDISPFSGDQ 15  
 Db 28 DNDIMPNSNGQ 39

RESULT 3

YF1Q\_ECOLI STANDARD; PRT; 886 AA.

ID YF1Q\_ECOLI  
 AC P76594; Q47320;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein yf1Q.

OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmatales;  
 OC Thermoplasmataceae; Thermoplasma.

OX NCBI\_TaxID=2303;

RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=DSM 1728;  
 RA MEDLINE:97426617; PubMed:9278503;  
 RA Blattner R.R.; Plunkett G. III.; Bloch C.A.; Perna N.T.; Burland V.;  
 RA Riley M.; Collado-Vides J.; Glasner J.D.; Mayhew G.F.;  
 RA Gregor J.; Davis N.W.; Kirkpatrick H.A.; Goeden M.A.; Rose D.J.;  
 RA Mau B.; Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2] \_  
 RP SEQUENCE OF 1-612 FROM N.A.  
 RC STRAIN=K12;  
 RA Nashimoto H.; Saito N.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.  
 CC -; SIMILARITY: SOME, IN THE N-TERMINAL, TO SUCCINYL-COA LIGASES.  
 CC -; SIMILARITY: STRONG, TO M.JANNASCHII MJ0590.  
 CC

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DR AE000344; AAC75637\_1; -;  
 DR EMBL; D64044; BAB10925\_1; -;  
 DR PIR; G65036; G65036.  
 DR EcoGene; EG14224; YF1Q.  
 DR InterPro; IPR03781; CoA-binding.  
 DR InterPro; IPR00182; GCN5acetyltransfer.  
 DR Pfam; PF00583; Acetyltransfer; 1.  
 DR Pfam; PF02629; CoA-binding; 1.  
 KW Hypothetical protein; Complete proteome.  
 FT CONFLICT 506 507 ST > YA (IN REF. 2).  
 SQ SEQUENCE 886 AA; 97987 MW; 255944B9E2961251 CRC64;

Query Match 50.0%; Score 41; DB 1; Length 886;  
 Best Local Similarity 70.0%; Pred. No. 40;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 DISPSEQDGQ 15  
 Db 693 DISPPEGDNE 702

RESULT 4

RUXX\_THEAC STANDARD; PRT; 83 AA.

ID RUXX\_THEAC  
 AC P57670;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative snRNP Sm-like protein.  
 GN TA1240.

OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasma.

OX NCBI\_TaxID=2303;

RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=DSM 1728;  
 RA MEDLINE:20479972; PubMed:11029001;  
 RA Ruepp A.; Graml W.; Santos-Martinez M.-L.; Koretke K.K.; Volker C.;  
 RA Newes H.-W.; Frishman D.; Stoerker S.; Lupas A.N.; Baumeister W.;  
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma  
 acidophilum.";  
 RT Nature 407:508-513 (2000).  
 RL

- SIMILARITY: Belongs to the snRNP Sm proteins family.

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CC EMBL; AL445067; CRC12364.1; - .  
 CC HAMAP; MF\_00257; ; 1.  
 CC DR InterPro; IPR006619; snRNP.  
 CC DR InterPro; IPR001163; snRNP\_Sm.  
 CC DR Pfam; PF01423; Sm; 1.  
 CC DR PRODOM; PD020287; snRNP; 1.  
 CC DR SMART; SM00051; Sm; 1.  
 CC DR Hypothetical protein; Ribonucleoprotein; Complete proteome.  
 KW Sequence 83 AA; 9070 MW; 07D132A75150864D CRC64;

Query Match Score 48.8%; DB 1; Length 393;  
 Best Local Similarity 66.7%; Pred. No. 4.2%; Indels 3; Gaps 1;  
 Matches 10; Conservative 0; Mismatches 2; Delins 0; Gaps 1;  
 Qy 2 RGDNDI--SPFSGPG 14  
 Db 68 RGDNIVFVPSKSGDG 82

## RESULT 5

GUNI\_USTMA ID\_GUNI\_USTMA STANDARD; PRT; 393 AA.  
 AC P54424;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)  
 DE (Cellulase 1) (EG 1).  
 GN EG1.  
 OS Ustilago maydis (Smut fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginaceae; Ustilago.  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BD11;

RX MEDLINE=96145728; PubMed=8590631;  
 RA Schauwecker F.; Wanner G.; Kahlmann R.;  
 RT "Filament-specific expression of a cellulase gene in the dimorphic  
 fungus *Ustilago maydis*";  
 RL *Biol. Chem.* Hoppe-Seyler 376:617-625(1995).  
 CC - CATALYTIC ACTIVITY: Endohydrolisis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - TISSUE SPECIFICITY: HYPER TIP.  
 CC - DEVELOPMENTAL STAGE: EXPRESSED IN FILAMENTOUS DIKARYON.  
 CC - PTM: MAY ALSO BE O-GLYCOSYLATED.  
 CC - SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL  
 HYDROLASES).

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CC EMBL; S81598; AAB26147.1; - .  
 CC DR HSSP; S5499; S59499.  
 CC DR InterPro; IPR000334; Glyco\_hydro\_45.  
 CC DR Pfam; PF02015; Glyco\_hydro\_45; 1.

CC DR PROSITE; PS01140; GLYCOSYL\_HYDROL; Hydrolase; Signal; Glycoprotein.  
 CC KW Cellulose degradation; Hydrolase; Glycosidase; Signal; Glycoprotein.  
 CC FT SIGNAL 1 26 POTENTIAL.  
 CC FT CHAIN 27 393  
 CC FT ACT SITE 34 34 NUCLEOPHILE (BY SIMILARITY).  
 CC FT ACT SITE 152 152 PROTON DONOR (BY SIMILARITY).  
 CC FT DOMAIN 385 385 ALA/GLY/SER/RICH.  
 CC FT CARBOHYD 343 343 N-LINED (GICNAAC... ) (POTENTIAL).  
 CC SQ SEQUENCE 393 AA; 39594 MW; 65C753C610CD6AD3 CRC64;

Query Match Score 48.8%; DB 1; Length 393;  
 Best Local Similarity 63.6%; Pred. No. 24;  
 Matches 7; Conservative 2; Mismatches 2; Delins 0; Gaps 0;  
 Qy 2 RGDNDI-SPFSG 12  
 Db 237 KDDNTISPYSG 247

## RESULT 6

ARGS\_KLBAE ID\_ARGS\_KLBAE STANDARD; PRT; 464 AA.  
 AC P20713; (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Arylsulfatase precursor (EC 3.1.6.1) (Aryl-sulfate sulphohydrolase).  
 GN ATSA.  
 OS Klebsiella aerogenes.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=28451; [1]  
 RN SEQUENCE FROM N.A., AND SIQUENCE OF 21-33.  
 RX MEDLINE=90202735; PubMed=2180918;  
 RA Murooka Y.; Ishibashi K.; Yasumoto M.; Sasaki M.; Sugino H.,  
 RA Azakami H.; Yamashita M.;  
 RT "A sulfur- and tyramine-regulated *Klebsiella aerogenes* operon  
 containing the arylsulfatase (atsB) gene and the atSB gene.";  
 RL J. Bacteriol. 172:2121-2140(1990).  
 CC - FUNCTION: AS IS COMMONLY PRODUCED BY SOIL MICROORGANISMS AND PLAYS  
 CC AN IMPORTANT ROLE IN THE MINERALIZATION OF SULFATES.  
 CC - CATALYTIC ACTIVITY: A phenol sulfate + H(2)O = a phenol + sulfate.  
 CC - SIMILARITY: BELONGS TO THE SULFATASE FAMILY.  
 CC

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 CC EMBL; M31938; AAC25051.1; - .  
 CC DR B35159; B35159.  
 CC DR InterPro; IPR00917; Sulfatase.  
 CC DR Pfam; PF00884; Sulfatase; 1.  
 CC DR PROSITE; PS010523; SULFATASE\_1; 1.  
 CC DR PROSITE; PS00149; SULFATASE\_2; 1.  
 CC KW Hydrolase; Signal; [1]  
 CC FT SIGNAL 21 20 ARYLSULFATASE.  
 CC FT ACT SITE 134 134 POTENTIAL.  
 CC SQ SEQUENCE 464 AA; 51471 MW; C8D09AB9E8F9C627 CRC64;

Query Match Score 48.8%; DB 1; Length 464;  
 Best Local Similarity 53.8%; Pred. No. 29;  
 Matches 7; Conservative 3; Mismatches 3; Delins 0; Gaps 0;  
 Qy 1 ERGDNDI-SPFSG 13  
 Db 35 DMGYSDISPFGGE 47

RESULT 7		FT	CONFLICT	202	G -> E (IN REF. 1).
MHD_ECOLI	STANDARD;	SQ	SEQUENCE	269 AA;	28890 MW; 34AB1A8A4B236358 CRC64;
ID	P77608; P71205; P7045;		Query Match	47.6%	Score 39; DB 1; Length 289;
AC	01-NOV-1997 (Rel. 35, Created)		Best Local Similarity	77.8%	Pred. No. 23;
DT	15-JUL-1998 (Rel. 36, Last sequence update)		Matches	7;	Mismatches 1; Indels 0; Gaps 0;
DT	15-SEP-2003 (Rel. 42, Last annotation update)	Qy	3 GNDISPER 11		
DF	2-keto-4-penoate hydratase (EC 4.2.1.7) (2-hydroxypentadienoic acid hydratase).		89 GDNEIIPRS 97		
DE		Db			
GN	MHPD OR B0350.				
OS	Escherichia coli.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
NCBI_TaxID	Enterobacteriaceae; Escherichia.				
OX					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / W3110;				
RA	Kawamukai M.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / CS52;				
RA	Ferrandez A., Garcia J.L., Diaz E.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / MG1655;				
RX	MEDLINE#200226617; PubMed=9278503;				
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mai B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474 (1997).				
RT					
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / MG1655;				
RA	Duncan M., Allen R., Araujo R., Aparicio A.M., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namith A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.				
RL	[5]				
RP	SEQUENCE OF 1-6, AND CHARATERIZATION				
RX	MEDLINE#98151237; PubMed=9432273;				
RA	Pollard J.R., Bugg T.D.; RT				
RT	"Purification, characterisation and reaction mechanism of monofunctional 2-hydroxypentadienoic acid hydratase from Escherichia coli."				
RT	Eur. J. Biochem. 251:98-106 (1998).				
CC	-!- COPFACTO: Requires a divalent metal ion for activity, optimum activity is obtained with Mn(2+).				
CC	-!- ENZYME REGULATION: Inhibited by sodium oxalate.				
CC	-!- PATHWAY: 3-hydroxypropionate degradation.				
CC	-!- SIMILARITY: BELONGS TO THE TODJ/XXLI/HPCG FAMILY.				
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DR	D8E239; BAA13055.1; .				
EMBL	Y09555; CAA07050.1; ALT_INIT.				
DR	AE000142; ANC73453.1; .				
DR	U73857; AAB18074.1; .				
DR	Ecogene:EG14274; mhpd.				
DR	InterPro:IPR002667; Hyratase decarb.				
DR	ProDom:PD003721; Hyratase decarb; 1.				
DR	Aromatic hydrocarbons catabolism; Lyase; Complete proteome.				
KW					



Db 69 EQSSEDLSFGNDG 82

RESULT 11			
DBP_SOUR	STANDARD;	PRT;	576 AA.
ID DBP_SOURCE_ID	(Rel. 29, Created)		
AC Q06801;	29, Last sequence update)		
DT 01-JUN-1994	(Rel. 29, Last sequence update)		
DT 16-OCT-2001	(Rel. 40, Last annotation update)		
DE 4-alpha-glucanotransferase, chloroplast precursor (EC 2.4.1.25)			
DE (Amylomaltase) (Disproportionating enzyme) (D-enzyme).			
GN DBP.			
OS Solanum tuberosum (Potato); Streptophytina; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicots; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Lamiidae; Solanales; Solanaceae; Solanum.			
OC NCBI_TAXID=4113;			
OX [1]			
RN			
RP SEQUENCE FROM N.A., AND SEQUENCE OF 53-57; 174-183 AND 247-259.			
RC STRAIN=cv. May Queen; TISSUE=Tuber;			
RX MEDLINE=93123262; Published=7678257;			
RA Takaha T., Yanase M., Okada S., Smith S.M., RT Disproportionating enzyme (4-alpha-glucanotransferase; EC 2.4.1.25) of potato. Purification, molecular cloning, and potential role in starch metabolism";			
RT starch metabolism";			
RL J. Biol. Chem. 268:1391-1396(1993).			
CC -!- FUNCTION: MAY ACT DURING STARCH BREAKDOWN TO CONVERT SMALL OLIGOSACCHARIDES INTO LARGER MOLECULES UPON WHICH STARCH PHOSPHORYLASE CAN ACT, OR MAY CHANGE THE STRUCTURE OF STARCH MOLECULES AND GRAIN ARCHITECTURE BY MODIFYING CHAIN LENGTH, OR MAY GENERATE FROM STARCH AND GLUCOSYL OLIGOSACCHARIDES WHICH CAN SERVE EITHER AS PRIMERS FOR NEW STARCH PHOSPHOENZYME.			
CC -!- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan to a new 4-position in an acceptor, which may be glucose or (1,4)-alpha-D-glucan.			
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OR AMYLOPLAST.			
CC -!- TISSUE SPECIFICITY: PRESENT IN LEAVES, ROOTS, AND STOLONS BUT IS MOST ABUNDANT IN DEVELOPING AND MATURE TUBERS.			
CC -!- SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.			
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CC EMBL; X88664; CAA88630.1; PIR; A45049; A45049.			
DR HSSP; OPI712; ICWY.			
DR InterPro; IPR03305; Glyco_Hydro_77.			
DR Pfam; PF02446; 4A_glycanotrans_1.			
DR TIGRFAMS; TIGR0027; malQ_1.			
KW Transferase; Glycosyltransferase; Carbohydrate metabolism; Amyloplast; Chloroplast; Transit Peptide.			
KW TRANSIT 1 52 CHLOROPLAST.			
FT CHAIN 53 576 4-ALPHA-GLUCANOTRANSFERASE.			
SQ SEQUENCE 576 AA; 64950 MW; AUD16FA546307BB CRC64;			
Query Match Score 39; DB 1; Length 576;			
Best Local Similarity 51.3%; Pred. No. 54; Indels 0; Gaps 0;			
Matches 7; Conservative 3; Mismatches 2; Mismatches 3; Conservative 3; Gaps 0;			
Qy 1 ERGDNDISPGSG 12			
Db 127 KRGNEDGSPYSG 138			
RESULT 12			
YP8_YEAST			
ID YP8_YEAST	STANDARD;	PRT;	612 AA.
Db 144 ERSSNENVSPFDE 156			
RESULT 13			
L2GL_DROPS			

ID	L2GL_DROPS	STANDARD;	PRT;	1166 AA.	
AC	Q08470; Q01-OCT-1994 (Rel. 30, Created)				
DT	01-OCT-1994 (Rel. 30, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Lethal(2) giant larva protein (P127).				
GN	L(2)GL.				
OS	Drosophila pseudoobscura (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriidae; Drosophilidae; Drosophiliidae.				
OX	NCBI_TaxID=7237;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAINS-Sprague-Dawley; TISSUE=Testis;				
RX	Medline=93390677; PubMed=390233;				
RA	Park S.H., Yoon J.H., Kwon Y.D., Park S.D.;				
RT	"Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II."				
RL	Biochem. Biophys. Res. Commun. 193:787-793 (1993).				
CC	-I- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II MAKES DOUBLE-STRAND BREAKS.				
CC	-I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.				
CC	-I- SUBUNIT: Homodimer.				
CC	-I- SUBCELLULAR LOCATION: Nuclear.				
CC	-I- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.				
CC	-I- SIMILARITY: Belongs to the type II topoisomerase family.				
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CC	-----				
CC	CC Mechler B.M.; "The L(2)gl homologue of Drosophila pseudoobscura suppresses tumorigenicity in transgenic Drosophila melanogaster."; Oncogene 8:1537-1549 (1993).				
RL	FUNCTION: CLOUD ACT AS TUMOR SUPPRESSOR.				
CC	-I- SUBUNIT: MAY FORM MULTIMERIC COMPLEXES.				
CC	-I- SUBCELLULAR LOCATION: CELLULAR MEMBRANE OR INTERCELLULAR MATRIX.				
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN THE EPITHELIAL CELLS OF THE DIGESTIVE TRACT AND IN GONADS, IN THE OVARY'S NURSE AND OOCYTE'S POLYLCHELIC CELLS.				
CC	-I- DEVELOPMENTAL STAGE: EXPRESSED ABUNDANTLY IN EARLY EMBRYOGENESIS.				
CC	MODERATE EXPRESSION IS FOUND IN LARVAL AND ADULT STAGES.				
CC	-I- DISEASE: MUTATIONS IN L(2)GL CAUSE MALIGNANT TRANSFORMATION OF THE OPTIC CENTRES OF THE LARVAL BRAIN AND THE IMAGINAL DISCS.				
CC	-----				
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CC	-----				
CC	EMBL; X73259; CAAE1715_1; -				
PIR	S31692; S37652;				
DR	FlyBase; FBgn001225; Dpsell(2)g1.				
DR	InterPro; IPR006634; Lethal(2) giant.				
DR	PRINTS; PR00562; DEATHL2GIANT.				
KW	Anti-oncogene; Repeat.				
FT	REPEAT 525 539 1.				
FT	REPEAT 615 629 2.				
SQ	SEQUENCE 1166 AA; 127216 MW; 815588AB45BD6AC6 CRC64;				
Query Match	47.6%; Score 39; DB 1; Length 1166;				
Best Local Similarity	58.3%; Pred. No. 1.2e+02;				
Matches	2; Mismatches 3; Indels 0; Gaps 0;				
Qy	1 ERGNDISPFSG 12				
Db	2886 QRGNDVIVFSG 297				
RESULT 14	{				
TPA_RAT	TPA_RAT STANDARD;	PRT;	1526 AA.		
AC	P41516;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	DNA topoisomerase II, alpha isoform (EC 5.99.1.3).				
GN	TOP2A OR TOP2 OR TOP-2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OC	NCBI_TaxID=10116;				
OX	[1]				
RN	[1]				
RESULT 15	{				
TP2A_MOUSE	TP2A_MOUSE STANDARD;	PRT;	1528 AA.		
ID	Q01320;				
AC	Q01320;				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	01-APR-1993 (Rel. 25, Last annotation update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	DNA topoisomerase II, alpha isoform (EC 5.99.1.3).				
GN	TOP2A OR TOP2 OR TOP-2.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OC	NCBI_TaxID=10090;				

RP SEQUENCE FROM N.A. PubMed=1331984;  
 RX MEDLINE=93065194;  
 RA Adachi N., Miyaike M., Ikeda H., Kikuchi A.;  
 RT "Characterization of cDNA encoding the mouse DNA topoisomerase II  
 that can complement the budding yeast top2 mutation.",  
 RL Nucleic Acids Res. 20:5297-5303 (1992).  
 RN [2].  
 RP SEQUENCE OF 1254-1528 FROM N.A.  
 RC TISSUE=Lymphoma;  
 RX MEDLINE=94084443; PubMed=8261398;  
 RA McPherson J., Brown G.A., Goldenberg G.J.;  
 RT "Characterization of a DNA topoisomerase IIalpha gene rearrangement  
 in adriamycin-resistant P388 leukemia expression of a fusion  
 messenger RNA transcript encoding topoisomerase IIalpha and the  
 retinoic acid receptor alpha locus.",  
 RT Cancer Res. 53:5885-5889 (1993).  
 CC -!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT  
 BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II  
 MAKES DOUBLE STRAND BREAKS.  
 CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 of double-stranded DNA.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH  
 CC NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES  
 CC RELAX ONLY NEGATIVE SUPERCOILS.  
 CC -!- SIMILARITY: Belongs to the type II topoisomerase family.  
 CC -----  
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 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; D12513; BAA02076.1; -;  
 DR EMBL; U01915; AAC5135.1; -;  
 DR PIR; JS0703; JS0703.  
 DR HSSP; PG6786; 1BGW.  
 DR MGDB; MG198790; Top2a.  
 DR InterPro; IPR003594; ATPbind\_Atpase.  
 DR InterPro; IPR003957; CBFA\_NFYB\_topois.  
 DR InterPro; IPR01241; DNA\_topoisotoli.  
 DR InterPro; IPR002205; DNA\_topoisotoli.  
 DR PFam; PF00204; DNA\_gyraseB; 1.  
 DR PFam; PF00521; DNA\_topoisomIV; 1.  
 DR PFam; PF02518; HATPase\_C; 1.  
 DR PRINTS; PR00615; CCAATSUBUNA.  
 DR PRINTS; PR00448; TP12\_FAMILY.  
 DR ProDom; PD000742; DNA\_topoisIV; 1.  
 DR SMART; SM00387; HATPase\_C; 1.  
 DR SMART; SM00433; TOP2C; 1.  
 DR SMART; SM00434; TOP4C; 1.  
 DR PROSITE; PS00177; TOPOISOMERASE\_II; 1.  
 KW Isomerate; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.  
 FT NP BIND 160 165 ATP (POTENTIAL).  
 FT ACT SITE 804 804 DNA CLEAVAGE (BY SIMILARITY).  
 SQ SEQUENCE 1528 AA; 172876 MW; 9061778DC46C756A CRC64;  
 Query Match 47.6%; Score 39; DB 1; Length 1528;  
 Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 GDNDISPPSGD 13  
 Db 201. GDMELKPFSGE 211





AC Q9ESO2;	DT 01-MAR-2001 (TREMBLrel. 16, Created)	QBK3V0 ID QBK3V0; PRELIMINARY;	PRT; 443 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		AC QBK3V0;	
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)		DT 01-OCT-2002 (TREMBLrel. 22, Created)	
DE Osteoregulin.		DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	
OS Rattus norvegicus (Rat).		DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Murinae; Rattus.		OS Rattus norvegicus (Rat)	
NCBI_TaxID=10116;		OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
RN [1]		NCBI_TaxID=0116;	
RP SEQUENCE FROM N.A.		RN [1]	
RC STRAIN=prague-Davley;		RP SEQUENCE FROM N.A.	
RX MEDLINEB2049633; PubMed=10967096;		RC STRAIN=P344;	
RA Petersen D.N., Tkalcovic G.T., Mansolff A.L., Rivera-Gonzalez R., Brown T.A.;		RA Wang X., Hu B., Wang Y.;	
RT "Identification of Osteoblast/Osteocyte Factor 45 (OF45), a Bone-Specific cDNA Encoding an RGD-containing Protein That Is Highly Expressed in Osteoblasts and Osteocytes.";		RT "Rattus norvegicus cDNA sequence expressed in B4 cell line (possible subtype of osteoregulin)"	
RT Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.		RT Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.	
DR AF53059; AAM94404.1; -		DR EMBL; AF53059; AAM94404.1; -	
RN [2]		SQ SEQUENCE 443 AA; 47672 MW; 7203EC4C0718FB14 CRC64;	
RP SEQUENCE FROM N.A.		Query Match 86.6%; Score 71; DB 11; Length 443;	
RC STRAIN=P344;		Best Local Similarity 85.7%; Pred. No. 0.00038;	
RA Hu B., Wang X., Wang Y.;		Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
RT "Rattus norvegicus cDNA sequence highly expressed in A1-5 cell line (identical to osteoregulin)"		Qy 2 RGDNIDSPSGDQ 15	
RT Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.		Db 177 RGDNIDVPFGDQ 190	
DR AF260922; AGG3336.1; -			
RN [3]			
SEQUENCE 435 AA; 46515 MW; D587FP82968A26BCB CRC64;			
RESULT 9			
Query Match 86.6%; Score 71; DB 11; Length 435;			
Best Local Similarity 85.7%; Pred. No. 0.00081;			
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy 2 RGDNIDSPSGDQ 15			
Db 169 RGDNIDVPFGDQ 182			
SEQUENCE 435 AA; 46515 MW; D587FP82968A26BCB CRC64;			
RESULT 7			
Query Match 86.6%; Score 71; DB 11; Length 435;			
Best Local Similarity 85.7%; Pred. No. 0.00081;			
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy 2 RGDNIDSPSGDQ 15			
Db 169 RGDNIDVPFGDQ 182			
SEQUENCE 435 AA; 46515 MW; D587FP82968A26BCB CRC64;			
RESULT 7			
Query Match 86.6%; Score 71; DB 11; Length 435;			
Best Local Similarity 85.7%; Pred. No. 0.00081;			
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy 2 RGK4L6 PRELIMINARY; PRT; 441 AA.			
DT 01-OCT-2002 (TREMBLrel. 22, Created)			
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DE Osteoregulin.			
GN MEB.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Gowen L.C., Peterken D.N., Vail A.L., Stock J., Tkalcevic G.T., Simmons H.A., Chidsey-Prink K.L., Ke H., McNeish J., Brown T.A.; RT Targeted disruption of the osteoregulin gene results in increased bone density";			
RT Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.			
DR AF298661; AM87687.1; -			
DR MGDP; MG12137384; Mepe.			
SEQUENCE 441 AA; 46672 MW; AA11947BFEE9F2E300 CRC64;			
Query Match 86.6%; Score 71; DB 11; Length 441;			
Best Local Similarity 85.7%; Pred. No. 0.00083;			
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy 2 RGDNIDSPSGDQ 15			
Db 183 RGDNIDVPFGDQ 190			
SEQUENCE 441 AA; 46672 MW; AA11947BFEE9F2E300 CRC64;			
RESULT 10			
Query Match 86.6%; Score 71; DB 11; Length 441;			
Best Local Similarity 85.7%; Pred. No. 0.00083;			
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy 2 RGDNIDSPSGF 12			
Db 246 RGDNIDSPFRG 257			
SEQUENCE 441 AA; 46672 MW; AA11947BFEE9F2E300 CRC64;			
RESULT 8			

GN CD209D OR SIGNR3.	ID Q9PQ03	PRELIMINARY;	PRT;	913 AA.
OS Mus musculus (Mouse).	AC Q9PQ03;			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	DT 01-OCT-2000 (TREMBLrel. 15, Created)			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
OX NCBI_TaxID=10090;	DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
RN [1]	DE N-terminal paralog.			
SEQUENCE FROM N.A.	GN UU487.			
RA STRAIN=C57BL/6;	OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).			
RA Park C.G.; Steinman R.M.; Bacterium; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.	OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.			
RT "Alternatively Spliced Forms of Mouse DC-SIGN Homologs.";	OC			
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	NCBI_TaxID=134821;			
RL [1]	RN [1]			
DR EMBL; A440280; AA133584; -.	RP SEQUENCE FROM N.A.			
DR MGJ:2157947; CD209d.	RC STRAIN=Serovar 3;			
DR InterPro; IPR001304; Anti-freezeII.	RX MEDLINE=2050219; PubMed=11049724;			
DR InterPro; IPR001304; Lectin C.	RA Glass J.J.; Lefkowitz E.J.; Glass J.S.; Heiner C.R.; Chen E.Y.,			
DR Pfam; PR00059; lectin C; 1.	RA Cassell G.H.; RT "The complete sequence of the mucosal pathogen Ureaplasma			
DR PRINTS; PR00356; ANTI-FREEZEII.	RT urealyticum."			
DR SMART; SM00034; CLECT; 1.	RL Nature 407:757-762 (2000).			
DR PROSITE; PS00615; C_TYPELECTIN_1; 1.	DR EMBL; AE002146; AAC030899; 1; -.			
DR PROSITE; PS50041; C_TYPELECTIN_2; 1.	KW Complete protein.			
SEQUENCE 207 AA; 23560 MW; 16FB4EB47ECAD3FB CRC64;	SQ SEQUENCE 913 AA; 106010 MW; FE9AD007C44AE0E3 CRC64;			
Query Match 54.9%; Score 45; DB 11; Length 207;	Query Match 54.9%; Score 45; DB 16; Length 913;			
Best Local Similarity 66.7%; Pred. No. 11;	Best Local Similarity 81.8%; Pred. No. 56;			
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy 3 GNDNISPFGDG 14	Qy 5 NDISPFSGDDQ 15			
Db 171 GDBDCAEFSGDG 182	Db 891 NDISPFSKDDQ 901			
RESULT 1.1	RESULT 13			
Q9IZWB	Q9VYY0	PRELIMINARY;	PRT;	793 AA.
OS Mus musculus (Mouse).	ID Q9VYY0			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	AC Q9VYY0;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DT 01-MAY-2000 (TREMBLrel. 13, Created)			
OX NCBI_TaxID=10090;	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
RN [1]	DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
SEQUENCE FROM N.A.	DE CG14085 protein.			
RA STRAIN=C57BL/6;	OS Drosophila melanogaster (Fruit fly).			
RA Pubmed=11581173;	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
RA Park C.G.; Takahara K.; Uemoto E.; Yashima Y.; Matsubara K.,	OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
RA Matsuda Y., Clusen B.E.; Inaba K.; Steinmann R.M.; Steimann R.M.;	OC Drosophila melanogaster; Drosophilidae; Drosophila.			
RT SIGNR3.	OC			
RA "Five mouse homologues of the human dendritic cell C-type lectin, DC-	OC			
RT SIGNR.";	NCBI_TaxID=7227;			
RA INT. Immunol. 13:1283-1290 (2001).	RN [1]			
RA DR EMBL; A4373411; AA132371; -.	RP SEQUENCE FROM N.A.			
RA DR MGJ:2157947; CD209d.	RC STRAIN=BERKELEY;			
RA InterPro; IPR001304; Lectin C.	RX MEDLINE=20196006; PubMed=10731132;			
RA Pfam; PR00059; lectin C; 1.	RA Adams M.D.; Celinker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.; Galle R.F.; George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.; Amantides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Bayraktaroglu L.; Beasley E.M.; Ballew R.M.; Basu A.; Baxendale J.; Bhandari D.; Bolshakov S.; Besson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Botchan M.R.; Bouck J.; Brokstein P.; Brottier P.; Borkova D.; Butler H.; Cadieu E.; Center A.; Chandra I.; Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.; de Pablo B.; Delcher A.; Deng Z.; Diaz A.D.; Dew I.; Dietz S.M.; Dodson K.; Douc L.E.; Downes M.; Dugan-Rocha S.; Ferriera S.; Fleischmann W.; Durbin R.K.; Evangelista C.C.; Fierro J.; Garg N.S.; Gelbart W.M.; Glasser K.; Fosler C.; Gabrialian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.; Glodek A.; Gong F.; Gorrell J.H.; Heiman T.J.; Hernández J.R.; Houck J.; Harris N.L.; Harvey D.; Heiman T.J.; Gu Z.; Guan P.; Harris M.; Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum R.A.; Kimmel B.E.; Kodira C.D.; Kraft C.; Lai Z.; Li J.; Li Y.; Liang Y.; Lin X.; Lasko P.; Lei Y.; Levitsky A.A.; Mcintosh T.C.; Mcleod M.P.; Mcpherson D.; Liu X.; Mattei B.;			
RA RESULT 1.2	Q9PQ03			
Qy 3 GNDNISPFGDG 14	Db 201 GDEDAEFSGDD 212			

RESULT 14  
 Q8Y183 PRELIMINARY; PRT; 277 AA.  
 ID Q8Y183;  
 AC 08Y183;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2003 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Lysezyme M1 precursor (BC 3.2.1.17).  
 GN BMEI0562.  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;  
 NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 OX NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
 OX NCBI\_TaxID=29461;  
 RA Daugherty S.C., Debroy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J.J., Malek J., Van Aken S.E.,  
 RA Redmiller S., Tettelin H., Gill S.R., White O., Salzberg S.B.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL EMBL; AE035171; AAU49175.1;  
 DR FlyBase; FBgn0036859; CG14085;  
 SQ SEQUENCE: FBgn0036859 CG14085 MW: FFC0E3DP3E57C41 CRC64;  
 Score 44.5; DB 5; Length 793;  
 Best Local Similarity 71.4%; Pred. No. 58;  
 Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 Qy 3 GDNDISPFGG-DGO 15  
 Db 693 GDNDISPFGQIQQQ 706

RESULT 14  
 Q8Y183 PRELIMINARY; PRT; 277 AA.  
 ID Q8Y183;  
 AC 08Y183;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2003 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Lysezyme M1 precursor (BC 3.2.1.17).  
 GN BMEI0562.  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;  
 NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13M / ATCC 23456 / Biotype 1;  
 RX MEDLINE=20201009; PubMed=11756688;  
 RA DelVecchio V.G., Redkar R.J., Patra G., Mujer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Renik G.,  
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,  
 RA Sellnow E., Elzer P.H., Hagiwara S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyriakis N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 Brucella melitensis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
 DR EMBL; AB009498; AAU51743.1;  
 DR InterPro: IPR002053; Glyco\_hydro\_25.  
 DR Pfam: PF01183; Glyco\_hydro\_25.1.  
 DR Prodom: PD004620; Glyco\_hydro\_25.1.  
 DR SMART: SR00641; Glyco\_25.1.  
 KW Hydrolase; Glycosidase; Complete proteome.  
 SQ SEQUENCE: FBgn0036859 CG14085 MW: FFC0E3DP3E57C41 CRC64;  
 Score 44.5; DB 5; Length 793;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 15  
 Q8F2N1 PRELIMINARY; PRT; 277 AA.  
 ID Q8F2N1;  
 AC 08F2N1;  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Glycosyl hydrolase, Family 25.  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Sieden-Klamos I., Simpson M.P., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner E., Venter R., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL EMBL; AE035171; AAU49175.1;  
 DR FlyBase; FBgn0036859; CG14085;  
 SQ SEQUENCE: FBgn0036859 CG14085 MW: FFC0E3DP3E57C41 CRC64;  
 Score 44.5; DB 5; Length 793;  
 Best Local Similarity 71.4%; Pred. No. 58;  
 Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Query Match 54.3%; Score 44.5; DB 5; Length 793;  
 Best Local Similarity 71.4%; Pred. No. 58;  
 Matches 10; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 3 GDNDISPFGG-DGO 15  
 Db 693 GDNDISPFGQIQQQ 706

Query Match 53.7%; Score 44; DB 16; Length 277;  
 Best Local Similarity 66.7%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RGDNIDSPFGGD 13  
 Db 252 RGDDADINTFGGD 263

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Result No.	Score	Query Match	Length	DB ID	Description	
1	126	100 0	23	AAU93726	Dental product bon C-terminal amide	
2	126	100 0	23	AAU93729	Dental product bon C-terminal amide	
3	126	100 0	97	AAU93681	Dental product bon C-terminal amide	
4	126	100 0	97	AAU93031	Protein of matrix Amino acid sequenc	
5	126	100 0	430	AAU93812	Truncated phosphat	
6	126	100 0	430	AAU93812	Human osteoregulin	
7	126	100 0	509	AAU93812	Human osteoregulin	
8	126	100 0	525	AAU93812	Phosphatotin polyp	
9	126	100 0	525	AAU93812	Human osteoregulin	
10	126	100 0	525	AAE13227	Human oncogenic O	
	11	126	100 0	525	AAE13227	Human osteoregulin
	12	126	100 0	540	AAU93923	Human osteoregulin
	13	126	100 0	556	AAU93923	Dental product bon
	14	101	80 2	40	AAU93703	Protein of matrix
	15	101	80 2	40	AAU93703	Human OOMI calcium
	16	86	68 3	19	AAE13230	Dental product bon
	17	84	66 7	15	AAU93725	C-terminal amidate
	18	84	66 7	15	AAU93725	Dental product bon
	19	84	66 7	3 3	AAU93710	Dental product bon
	20	84	66 7	3 3	AAU93710	Peptide of matrix
	21	82	65 1	15	AAU93724	Dental product bon
	22	82	65 1	15	AAU93724	C-terminal amidate
	23	81	64 3	435	AAU93718	Rat osteoregulin
	24	81	64 3	441	AAU93719	Mouse osteoregulin
	25	80	63 5	275	AAU93507	Human polypeptide
	26	75	59 5	15	AAU93723	Dental product bon
	27	75	59 5	15	AAU93723	C-terminal amidate
	28	73 5	58 3	40	AAU93704	Dental product bon
	29	73 5	58 3	40	AAU93704	Protein of matrix
	30	72 5	57 5	30	AAU93706	Dental product bon
	31	72 5	57 5	30	AAU93706	Peptide of matrix
	32	72 5	57 5	35	AAU93705	Dental product bon
	33	72 5	57 5	35	AAU93705	Peptide of matrix
	34	66	52 4	1 2	AAU93722	Peptide of a calc
	35	57	45 2	40	AAU93712	Dental product bon
	36	57	45 2	40	AAU93712	Protein of matrix
	37	57	45 2	45	AAU93707	Dental product bon
	38	57	45 2	45	AAU93707	Protein of matrix
	39	53	42 1	10 9	AAE13214	Human bone marrow
	40	53	42 1	1 7	ABP3356	Human phospholipid
	41	53	42 1	12 16	AAE23860	Human phospholipid
	42	53	42 1	14 58	ABD9355	Human lipase NHL
	43	53	42 1	14 58	ABD93556	Human lipase NHL
	44	53	42 1	14 58	AAE34440	Human lipid-assoc
	45	52	41 3	19	AAE13229	Human porin peptid
					ALIGNMENTS	
					RESULT 1 AAU93726	
					ID AAU93726 standard; peptide; 23 AA.	
					XX	
					AC AAU93726;	
					XX	
					DT 02-JUL-2002 (first entry)	
					XX	
					DE Dental product bone growth enhancing peptide #46.	
					XX	
					DR Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.	
					XX	
					OS Synthetic.	
					XX	
					PN WO200213775-A1.	
					XX	
					PD 21-FEB-2002.	
					XX	
					PF 09-AUG-2001; 2001WO-US25101.	
					XX	
					PR 16-AUG-2000; 2000US-225879P.	
					XX	
					(BIG-) BIG BEAR BIO INC.	
					PA XX	
					PY Yoneda T, Nomizu M, Kumagai Y;	
					XX	
					DR WPI; 2002-329525/36.	
					XX	
					PT Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific	

PT amino acid in a sequence containing the integrin binding motif -  
 XX  
 PS Claim 7; Page 21; 44pp; English.

The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU93681-AAU93726 represent bone growth enhancing peptides for use in dental products.

XX Sequence 23 AA;  
 Query Match 100.0%; Score 126; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2e-12; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0;  
 QY 1 TDLOERGNDNDISPFSGDQQFKD 23  
 Db 1 TDLOERGNDNDISPFSGDQQFKD 23

RESULT 3  
 AAU93681.  
 ID AAU93681 standard; protein; 97 AA.  
 XX  
 AC AAU93681;  
 XX  
 DT 02-JUL-2002 (first entry)

Query Match 100.0%; Score 126; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2e-12; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0;  
 QY 1 TDLOERGNDNDISPFSGDQQFKD 23  
 Db 1 TDLOERGNDNDISPFSGDQQFKD 23

RESULT 2  
 AAU93681 standard; peptide; 23 AA.  
 ID AAU93681  
 XX  
 AC AAU93681;  
 XX  
 DT 31-MAY-2002 (first entry)

DE C-terminal amidated synthesised peptide D-00006.

XX Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; D00006.

OS Synthetic.

PH Key Location/Qualifiers  
 FT Modified-site 23  
 PT /note= "C-terminal amide"  
 XX  
 PN WO200214360-A1.

PD 21-FEB-2002.  
 XX  
 PF 14-AUG-2001; 2001WO-US25542.  
 XX  
 PR 16-AUG-2000; 2000US-0641034.  
 XX  
 PR 19-MAR-2001; 2001US-0812485.  
 XX  
 PA (BIGB-) BIG BEAR BIO INC.

XX  
 PI Kumagai Y, Blacher RW, Yoneda T;

XX  
 DR WPI; 2002-291971-33.

New Peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, a glycosaminoglycan binding motif or a calcium binding motif -  
 XX  
 PS Example 1; Page 15; 50pp; English.

The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding

motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a C-terminal amidated synthesised peptide D-00006 of the invention.

XX Sequence 23 AA;  
 Query Match 100.0%; Score 126; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2e-12; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0;  
 QY 1 TDLOERGNDNDISPFSGDQQFKD 23  
 Db 1 TDLOERGNDNDISPFSGDQQFKD 23

RESULT 3  
 AAU93681.  
 ID AAU93681 standard; protein; 97 AA.  
 XX  
 AC AAU93681;  
 XX  
 DT 02-JUL-2002 (first entry)

XX Dental product bone growth enhancing Peptide #1.

XX DE Dental product; toothpaste; mouthwash; dental floss; bone growth; KW integrin binding motif; RGD; skeletal disease; tooth; tooth; KW alveolar bone growth; osteoblast; odontoblast; osteopathic.

XX Synthetic.

XX OS  
 PN WO200213775-A1.  
 XX PD 21-FEB-2002.  
 XX PF 09-AUG-2001; 2001WO-US25101.  
 XX PR 16-AUG-2000; 2000US-225879P.  
 XX PA (BIGB-) BIG BEAR BIO INC.  
 XX PI Yoneda T, Nomizu M, Kumagai Y;  
 XX DR WPI; 2002-329525/36.

XX Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif -

XX Disclosure; Page 11; 44pp; English.

XX  
 PT  
 CC The present invention relates to dental products such as toothpastes, CC mouthwash and dental floss comprising a base material and a compound CC which promotes bone growth. Such compounds are peptide sequences CC comprising 10-50 amino acids and containing an integrin binding CC motif such as RGD in the D- or L- form, preferably the L-configuration. CC The peptides of the invention are useful for treating or preventing CC skeletal diseases such as dental disease. The peptides enhance tooth CC and/or alveolar bone growth on areas where deterioration has occurred, CC as well as the growth or recruiting of osteoblast or odontoblast cells CC on the surface of the new skeletal growth. AAU93681-AAU93726 represent CC bone growth enhancing peptides for use in dental products.

XX Sequence 97 AA;

Query Match 100.0%; Score 126; DB 23; Length 97;  
 Best Local Similarity 100.0%; Pred. No. 1.e-11; Indels 0; Gaps 0;

Qy	1	TDLQERGNDIDISPFSGDCQPFKD	23		XX	DT	22-FEB-2000	(first entry)
Db	43	TDLQERGNDIDISPFSGDCQPFKD	65		XX	DE	Amino acid sequence of a human phosphatotin polypeptide.	
	RESULT 4				XX			
	AAQ20331				KW	Human; phosphatotin; Metastatic-tumour Excreted Phosphaturic-Element;		
	ID AAQ20331 standard; protein; 97 AA.				KW	MEPE; Na+-dependent phosphatase; vitamin D metabolism;		
	XX				KW	bone mineralisation; phosphate metabolism related disease;		
	AC AAQ20331;				KW	hyperphosphatemia; renal osteodystrophy; renal dialysis;		
	XX				KW	secondary hyperparathyroidism; osteitis fibrosa cystica; hypercalcemia;		
	AC				KW	X-linked hypophosphatemic rickets; hereditary hypophosphatemic ricket;		
	XX				KW	hypomineraled bone lesion; stunted growth; Cystic Fibrosis;		
	DT 31-MAY-2002 (first entry)				KW	oncogenic hypophosphatemic osteosarcoma; renal phosphate leakage;		
	XX				KW	renal osteodystrophy; osteoporosis; Vitamin D resistant rickets;		
	DE Protein of matrix extracellular phosphoglycoprotein containing RGD #1.				KW	end organ resistance; renal Fanconi syndrome; rickets;		
	XX				KW	Page's disease; kidney failure; renal tubular acidosis; sprue.		
	DE				XX			
	XX				XX	Homo sapiens.		
	XX				Key			
	XX				Modified-site			
	OS Unidentified.				FT	FT	/note= "protein kinase C phosphorylation site"	
	XX				FT	FT	8..10	
	PN WO200214360-A1.				FT	FT	8..11	
	XX				FT	FT	/note= "Casein kinase II phosphorylation site"	
	PD 21-FEB-2002.				FT	FT	16..21	
	XX				FT	FT	/note= "myristoylation site"	
	XX				FT	FT	40..47	
	PF 14-AUG-2001; 2001WO-US25542.				FT	FT	/note= "Tyrosine kinase phosphorylation site"	
	XX				FT	FT	77..79	
	PR 16-AUG-2000; 2000US-0641034.				FT	FT	/note= "protein kinase C phosphorylation site"	
	PR 19-MAR-2001; 2001US-0812485.				FT	FT	118..120	
	XX				FT	FT	/note= "protein kinase C phosphorylation site"	
	PA (BIGB-) BIG BEAR BIO INC.				FT	FT	119..124	
	XX				FT	FT	/note= "myristoylation site"	
	PI Kumagai Y, Blacher RW, Yoneda T;				FT	FT	139..142	
	XX				FT	FT	/note= "Casein kinase II phosphorylation site"	
	DR 2002-291971/33.				FT	FT	143..148	
	XX				FT	FT	/note= "myristoylation site"	
	PT New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif.				FT	FT	152..154	
	PT Glycosaminoglycan binding motif or a calcium binding motif -				FT	FT	/note= "cell attachment tripeptide"	
	XX				FT	FT	161..165	
	PS Disclosure; Page 11; 50PP; English.				FT	FT	/note= "glycosaminoglycan attachment site"	
	XX				FT	FT	177..180	
	CC The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L-conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and/or reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.				FT	FT	194..197	
	CC				FT	FT	/note= "Casein kinase II phosphorylation site"	
	CC				FT	FT	199..202	
	CC				FT	FT	/note= "Casein kinase II phosphorylation site"	
	CC				FT	FT	203..205	
	CC				FT	FT	/note= "protein kinase C phosphorylation site"	
	CC				FT	FT	224..227	
	CC				FT	FT	/note= "Casein kinase II phosphorylation site"	
	CC				FT	FT	228..231	
	CC				FT	FT	/note= "Casein kinase II phosphorylation site"	
	CC				FT	FT	228..230	
	CC				FT	FT	/note= "protein kinase C phosphorylation site"	
	CC				FT	FT	238..241	
	XX				FT	FT	/note= "Casein kinase II phosphorylation site"	
	SQ Sequence 97 AA;				FT	FT	266..271	
	Query Match 100.0%; Score 126; DB 23; Length 97;				FT	FT	/note= "myristoylation site"	
	Best Local Similarity 100.0%; Pred. No. 1..1e-11; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				FT	FT	291..296	
	Db 1. TDLOERGNDIDISPFSGDCQPFKD 23				FT	FT	/note= "myristoylation site"	
	Db 43 TDLOERGNDIDISPFSGDCQPFKD 65				FT	FT	311..313	
	RESULT 5				FT	FT	/note= "protein kinase C phosphorylation site"	
	AAV53812				FT	FT	312..314	
	ID AAV53812 standard; Protein; 430 AA.				FT	FT	/note= "protein kinase C phosphorylation site"	
	XX				FT	FT	315..320	
	AC AAV53812;				FT	FT	/note= "myristoylation site"	
					FT	FT	319..321	
					FT	FT	/note= "protein kinase C phosphorylation site"	
					FT	FT	325..328	
					FT	FT	/note= "Casein kinase II phosphorylation site"	
					FT	FT	370..373	

PT	Modified-site	/note= "amidation site"	Qy	1 TDHQERGDNDISPFSGDQQPKD 23
PT	Modified-site	/note= "Asu-glycosylation site"	Db	147 TDHQERGDNDISPFSGDQQPKD 169
FT	Modified-site	383..387		
FT	Modified-site	384..386		
FT	Modified-site	/note= "protein kinase C phosphorylation site"		RESULT 6
FT	Modified-site	/note= "myristoylation site"	ID	AAB62669 standard; Protein: 430 AA.
FT	Modified-site	403..405	XX	
FT	Modified-site	405..408	XX	
FT	Modified-site	/note= "cAMP and cGMP dependent protein kinase phosphorylation site"	AC	AAB62669;
FT	Modified-site	408..410	DT	23-JUL-2001 (first entry)
FT	Modified-site	/note= "protein kinase C phosphorylation site"	DE	Truncated phosphatoin polypeptide (truncated MEPE).
FT	Modified-site	409..411	XX	
FT	Modified-site	/note= "protein kinase C phosphorylation site"	KW	Metastatic-tumour excreted phosphaturic element; MEPE; phosphatoin;
FT	Modified-site	422..426	KW	phosphate; vitamin-D; skeletal formation; mineralization; truncated;
FT	Modified-site	/note= "Cassein kinase II phosphorylation site"	KW	osteopathic; antigout; cytostatic; human.
FT	Modified-site	425..428	XX	
FT	Modified-site	/note= "Cassein kinase II phosphorylation site"	OS	Homo sapiens.
FT	Modified-site	427..430	XX	
FT	Modified-site	/note= "Cassein kinase II phosphorylation site"	PH	
XX	W09560017-A2.		FT	Misc-difference 161..192
XX			FT	/note= "the amino acid residues in this region are indicated incorrectly in the sequence listing"
PD	25-NOV-1999.		FT	in the sequence listing"
XX			XX	WO200132878-A2.
PF	18-MAY-1999;	99WO-EP03403.	XX	
XX			PD	10-MAY-2001.
PR	18-MAY-1998;	98GB-00-010681.	XX	
PR	04-SEP-1998;	98GB-00-19387.	PF	31-OCT-2000; 2000WO-EP10747.
XX	(UNLO ) UNIV COLLEGE LONDON.		XX	
PA			PR	04-NOV-1999; 99US-0434185.
XX	Rowe P;		PR	08-NOV-1999; 99GB-0026424.
PI			XX	(UNLO ) UNIV COLLEGE LONDON.
XX	WPI: 2000-053262/04.		PA	
DR	N-PSDB; AAZ36447.		XX	
XX	New polypeptides involved in the regulation of phosphate metabolism useful for diagnosing and treating disorders related to phosphate metabolism		PI	Rowe P;
PT			XX	WPI: 2001-343487/36.
PT			DR	N-PSDB; AAF33759.
PT			PT	New phosphatoin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, for skeletal formation e.g. osteoporosis, Paget's disease, gout -
XX			PT	
PS	Claim 6; Fig 8; 13pp; English.		XX	
XX	The present sequence represents a phosphatoin polypeptide (also called Metastatic-tumour Excreted Phosphaturic-Element (MEPE)). The level of phosphatoin in a subject modulates Na+-dependent phosphate cotransport, vitamin D metabolism and/or bone mineralisation. The phosphatoin polypeptides, polynucleotides, vectors and antibodies are used to treat or prevent hypophosphataemia, or renal osteodystrophy, hyperphosphataemia in renal dialysis/pre-dialysis, secondary hyperparathyroidism or osteitis fibrosa cystica, or X-linked hypophosphataemic rickets, hereditary hypophosphataemic bone lesions, stunted growth in juveniles, oncogenic hypophosphataemic osteomalacia, renal phosphate leakage, renal osteodystrophy, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide may also be used to manufacture combined preparations for simultaneous separate or sequential use for the treatment of phosphate metabolism disorders. A transformed osteoblast or bone cell line capable of phosphatoin overexpression is useful for the production of phosphatoin.		PS	Claim 4; Fig 8; 13pp; English.
CC	Sequence 430 AA;		XX	The invention relates to a novel human protein, metastatic-tumour excreted phosphaturic element (MEPE) or phosphatoin (modulator of phosphate and vitamin-D metabolism). The phosphatoin polypeptides, polynucleotides and specific antibodies are useful for treating a disorder of phosphate or vitamin D metabolism, skeletal formation and mineralization. Phosphatins are used to treat hyperphosphataemia, renal osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica or gout. It is used to prepare a medicament for treating X-linked hypophosphataemic rickets, hereditary hypophosphataemic rickets with hypercalcauria (HHRH), hypomineralised CC
CC	CC		CC	hypophosphataemic rickets, end organ resistance, renal osteodystrophy, CC
CC	CC		CC	osteoporosis, vitamin D resistant rickets, end organ resistance, renal CC
CC	CC		CC	osteoporosis, vitamn D syndrome, autosomal rickets, Paget's disease, kidney failure, CC
CC	CC		CC	Fanconi syndrome, autosomal rickets, renal osteodystrophy, osteomalacia, renal phosphate CC
CC	CC		CC	leakage, renal osteodystrophy, osteoporosis, vitamin-D resistant rickets, CC
CC	CC		CC	end organ resistance, renal Fanconi syndrome, autosomal rickets, phosphate CC
CC	CC		CC	disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide CC
CC	CC		CC	polypeptides are useful for detecting the presence of a specific mRNA. Phosphatoin polypeptides are also useful for identifying CC
CC	CC		CC	antagonists and antagonists, compounds which bind to phosphate CC
CC	CC		CC	metabolism. The present sequence represents a truncated form of phosphate CC
CC	CC		CC	disorders. The present sequence represents a truncated form of phosphate CC
XX	SQ		XX	phosphatoin (MEPE).
Sequence	430 AA;		Sequence	430 AA;





XX Human oncogenic osteomalacia-related protein-1 (OOM-1).  
DE OOM1 is useful as an immunogen to produce antibodies against  
XX OOM1 and in vitro assays to screen for agents or drugs which modulate  
CC cellular processes. The present sequence is human oncogenic  
CC osteomalacia-related protein-1 (OOM-1).  
CC Note: The present sequence states that this sequence is encoded by the  
CC DNA sequence shown in SEQ ID NO: 1 (AAD21889) of the specification.  
KW However this does not appear to be the case.

XX SQ Sequence 525 AA;

XX Key Location/Qualifiers 100 0%; Score 126; DB 23; Length 525;  
PH 1.16 Best Local Similarity 100.0%; Pred. No. 7.3e-11;  
FT /label= Signal\_Peptide  
FT 17..525 Matches 23; Conservative 0; Mismatches 0; Index 0; Caps 0;  
FT /note= "Mature oncogenic osteomalacia-related protein-1 (OOM-1)"  
FT Domain 130..142 Qy 1 TDLQERDDNDISPESGQDQPKFD 23  
FT FT 235..258 Db 242 TDLQERDDNDISPESGQDQPKFD 264

FT /note= "Calcium binding motif"  
FT Region 247..249 RESULT 12  
FT Domain 264..275 AAB8293 standard; Protein; 540 AA.  
FT /note= "Cell attachment site"  
FT /note= "Calcium binding motif"  
FT Domain 412..424 AC AAB8293;  
FT /note= "Calcium binding motif"  
FT Modified-site 442..455 DT 21-DEC-2001 (first entry)  
DE Human osteoregulin (mature polypeptide).  
FT /note= "Potential PKA phosphorylation site"  
FT Modified-site 477..481 XX  
FT /note= "Glycosylation site"  
FT Domain 500..503 KW Osteoregulin; human; bone; homeostasis; adipose; calcification;  
FT /note= "Bacterial extracellular solute-binding KW atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;  
FT protein motif"  
XX KW therapy.  
XX OS Homo sapiens.  
XX PN EP1130098-A2.  
XX PD XX  
XX PD 05-SEP-2001.  
XX PF XX  
XX PR 27-FEB-2001; 2001EP-0301768.  
XX PR XX  
XX PR 29-FEB-2000; 2000US-185617P.  
XX PR 22-SEP-2000; 2000US-234500P.  
XX PA XX  
XX PA (PFIZ ) PFIZER PROD INC.  
XX PI Brown TA, De Wet JR, Gowen LC, Hames LM;  
XX DR WPI; 2001-604111/69.  
XX DR N-PSDB; AAB26811.

XX PS Claim 1; Page 59-61; 90pp; English.

XX The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence.  
CC Osteoregulin is a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin were identified (see also AAB82922). The invention provides novel osteoregulin proteins, nucleic acids which express heterologous osteoregulins, and antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification polymorphisms which are mutants, variants of the gene in human

XX New polynucleotide encoding a polypeptide useful for identifying polyamide or polypeptide activity modulators used for treating oncogenic osteomalacia. Comprises the oncogenic osteomalacia-related gene -  
XX  
XX PS Claim 2; Fig 2; 65pp; English.

XX The invention relates to oncogenic osteomalacia-related protein 1 designated OOM1 (oncogenic osteomalacia-related factor) and its DNA molecule. OOM1 protein is useful for treating a phosphate homeostasis-related disease such as X-linked hypophosphatasia, rickets, oncogenic osteomalacia, rhabdomyolysis, cardiomyopathy, tumoural calcinosis and renal failure. OOM1 proteins and DNA's are useful for modulating the phenotype of a neoplastic cell associated with oncogenic osteomalacia; modulating bone mineralisation; treating a disease characterised by abnormal bone mineralisation; and treating an oncogenic osteomalacia-associated symptom such as hypophosphataemia, phosphaturia, low serum concentrations of 1,25-dihydroxy vitamin D or osteomalacia. OOM1 is useful for modulating renal phosphate transport, which involves altering the activity of OOM1 within a cell and than administering serine protease 11 to the cell. OOM1 DNA is useful for generating non-human transgenic animal models, and for searching and identifying single nucleotide polymorphisms which are mutants, variants of the gene in human

CC (claimed), for treating and preventing osteoporosis, and for  
CC stimulating bone repair and regeneration.

XX SQ Sequence 540 AA;

Query Match	100.0%	Score 126;	DB 22;	Length 540;
Best Local Similarity	100.0%	Pred. No.	7.6e-11;	
Matches	23;	Conservative	0;	Indels 0; Gaps 0;

Qy 1 TDLOERGNDNDISPFSGDQQPKD 23  
Db 257 TDLOERGNDNDISPFSGDQQPKD 279

## RESULT 13

AAB82921 standard; Protein; 556 AA.

XX AC AAB82921;  
XX DT 21-DEC-2001 (first entry)  
XX DB Human osteoregulin.  
XX KW Osteoregulin; human; bone; homeostasis; adipose; calcification; atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic; therapy.  
XX KW Homo sapiens.  
XX FH Key Peptide 1.37  
FT /label= Signal\_peptide  
FT Protein 3B .556  
FT /label= Mature\_protein  
FT Misc-difference 57  
FT /note= "Encoded by TCA"  
PN EP1130098-A2.  
XX PD 05-SEP-2001.  
XX PF 27-FEB-2001; 2001EP-0301768.  
XX PR 29-FEB-2000; 2000US-185617P.  
XX PR 22-SEP-2000; 2000US-234500P.  
XX PA (PFIZER PROD INC.  
XX PI Brown TA, De Wet JR, Gowen LC, Hames LM;  
XX WPI; 2001-60411/69.  
XX DR N-PDB; AAH26809.

XX Novel osteoregulin polypeptide useful for regulating bone homeostasis, PT adipoxyd and calcification of atherosclerotic plaques comprises PT measuring the activity of osteoregulin -  
XX Claim 1; Page 48-49; 90pp; English.

XX The present sequence is that of human osteoregulin, a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. The sequence is predicted from the nucleotide sequence (see AAH6809) of isolated osteoblast cDNA. A splice variant of human osteoregulin was also identified (see AAH82920). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful

CC in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.

XX SQ Sequence 556 AA;

Query Match	100.0%;	Score 126;	DB 22;	Length 556;
Best Local Similarity	100.0%;	Pred. No.	7.8e-11;	
Matches	23;	Conservative	0;	Indels 0; Gaps 0;

Qy 1 TDLOERGNDNDISPFSGDQQPKD 23  
Db 273 TDLOERGNDNDISPFSGDQQPKD 295

RESULT 14

AAU93703	ID AAU93703 standard; peptide; 40 AA.
XX AC AAU93703;	XX DT 02-JUL-2002 (first entry)
XX DE Dental product bone growth enhancing peptide #23.	XX KW Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
XX OS Synthetic.	XX PN WO200213775-A1.
XX PR 21-FEB-2002.	XX PD 09-AUG-2001; 2001WO-US25101.
XX PF 16-AUG-2000; 2000US-225879P.	XX PA (BIGB-) BIG BEAR BIO INC.
XX DR WII; 2002-329525/36.	XX PI Yoneda T, Nomizu M, Kumagai Y;
XX PS Claim 6; Page 20; 44pp; English.	XX CC The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L-form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU93681-AAU93726 represent sequence 40 AA;
XX SQ Query Match 80.2%; Score 101; DB 23; Length 40;	XX CC Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 6 RGDNIDSPFSGDQQPKD 23

Db 1 RGDNIDSPFSGDQQPKD 18

RESULT 15  
 AAC20353  
 ID AAC20353 standard; protein; 40 AA.  
 XX  
 AC AAC20353;  
 XX 31-MAY-2002 (first entry)  
 XX DB Protein of matrix extracellular phosphoglycoprotein containing RGD #23.  
 XX KW Bone growth; RGD motif; integrin binding motif; calcium binding motif;  
 XX glycosaminoglycan binding motif; bone loss; renal phosphate excretion;  
 XX alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;  
 XX weakness; matrix extracellular phosphoglycoprotein.  
 XX OS Unidentified.  
 XX PN WO200213360-A1.  
 XX PD 21-FEB-2002.  
 XX PF 14-AUG-2001; 2001WO-US25542.  
 XX PR 16-AUG-2000; 2000US-0611034.  
 PR 19-MAR-2001; 2001US-0812485.  
 XX PA (BIGB-) BIG BEAR BIO INC.  
 XX PI Kumagai Y, Blacher RW, Yoneda T;  
 XX DR 2002-291971/33.

XX New peptide compound useful for reducing bone loss, is capable of  
 PT enhancing bone growth, and comprises an integrin binding motif,  
 PT glycosaminoglycan binding motif or a calcium binding motif.  
 XX Disclosure: Page 12: 50PP; English.

XX The invention relates to a peptide compound capable of enhancing bone  
 CC growth, and comprising 10-50 amino acids in a sequence, where the amino  
 CC acids are in D- or L- conformation and the sequence comprises a motif  
 CC selected from an integrin binding motif, a glycosaminoglycan binding  
 CC motif and a calcium binding motif. The peptide of the invention is useful  
 CC for reducing bone loss and for reducing renal phosphate excretion in an  
 CC individual. The peptide is useful for promoting regeneration of alveolar  
 CC bone and/or teeth, and increases the number and activity of odontoblasts  
 CC /osteoclasts that help form dental tissues. The peptide is also useful  
 CC for treating or preventing a condition associated with skeletal loss or  
 CC weakness. This sequence represents a protein of a matrix extracellular  
 CC phosphoglycoprotein containing an RGD motif of the invention.

XX Sequence 40 AA;

Query Match 80.2%; Score 101; DB 23; Length 40;

Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 RGDNIDSPFSGDQQPKD 23  
 Db 1 RGDNIDSPFSGDQQPKD 18

Search completed: January 29, 2004, 12:38:35  
 Job time : 43.9737 secs

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Result No.	Score	Query	Match	Length	DB ID	Description
1	52	41.3	301	2	US-08-355-844-2	Sequence 2, Appli
2	52	41.3	301	5	PCT-US95-16126-2	Sequence 2, Appli
3	47	37.3	815	4	US-09-134-001-C-3614	Sequence 3614, Ap
4	47	37.3	1198	4	US-09-199-637A-405	Sequence 405, Ap
5	46	36.5	425	4	US-09-252-991A-31834	Sequence 31834, A
6	45.5	36.1	96	2	US-08-341-843B-9	Sequence 9, Appli
7	45.5	36.1	96	2	US-08-427-497E-14	Sequence 14, Appli
8	45.5	36.1	101	4	US-09-252-991A-22899	Sequence 22899, A
9	45.5	36.1	1260	4	US-08-506-296B-21	Sequence 21, Appli
10	45	35.7	547	4	US-09-252-991A-32044	Sequence 32044, A
11	44	34.9	186	4	US-09-328-352-7703	Sequence 7703, Ap
12	44	34.9	348	1	US-08-176-126B-2	Sequence 2, Appli
13	44	34.9	348	2	US-08-669-435-2	Sequence 2, Appli
14	44	34.9	348	5	PCT-US94-14431A-2	Sequence 2, Appli
15	44	34.9	475	1	US-08-278-091-6	Sequence 6, Appli
16	44	34.9	475	1	US-08-483-859-6	Sequence 6, Appli
17	44	34.9	475	1	US-08-472-173-6	Sequence 6, Appli
18	44	34.9	475	1	US-08-350-741-2	Sequence 2, Appli
19	44	34.9	475	2	US-08-487-167-6	Sequence 6, Appli
20	44	34.9	475	2	US-08-482-816-6	Sequence 6, Appli
21	44	34.9	475	2	US-08-296-149-6	Sequence 6, Appli
22	44	34.9	475	2	US-08-801-499-6	Sequence 6, Appli
23	44	34.9	475	2	US-08-463-775A-2	Sequence 2, Appli
24	44	34.9	475	2	US-08-615-271-6	Sequence 6, Appli
25	44	34.9	475	3	US-09-074-660-6	Sequence 6, Appli
26	44	34.9	475	3	US-09-074-659-6	Sequence 6, Appli
27	44	34.9	475	3	US-09-106-468-6	Sequence 6, Appli

Query Match      41.3%;    Score 52;    DB 2;    Length 301;  
 Best Local Similarity      58.8%;    Pred. No. 3.6;  
 Matches 10;    Conservative 2;    Mismatches 5;    Indels 0;    Gaps 0;

RESULT 2  
 PCT-US95-16126-2  
 ; Sequence 2, Application PC/TUSS9516126  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: Fischbarg, Jorge  
 ;    Czeigledy, Ferenc  
 ;    Isarovitch, Pavel  
 ;    Li, Jun  
 ;    APPLICANT: Cheung, Min  
 ;    TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
 ;    NUMBER OF SEQUENCES: 3  
 ;    CORRESPONDENCE ADDRESS:  
 ;    ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
 ;    STREET: 30 Rockefeller Plaza  
 ;    CITY: New York  
 ;    STATE: NY  
 ;    COUNTRY: USA  
 ;    ZIP: 10112-0228  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: PCT/US95/16126  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ;    APPLICATION NUMBER: US 08/355, 844  
 ;    FILING DATE: 14-DEC-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ;    NAME: Tang, Henry Y. S.  
 ;    REGISTRATION NUMBER: 29,705  
 ;    REFERENCE/DOCKET NUMBER: A29927-50/29910  
 ; TELECOMMUNICATION INFORMATION:  
 ;    TELEPHONE: 212-408-2586  
 ;    TELEFAX: 212-765-2519  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ;    SEQUENCE CHARACTERISTICS:  
 ;    LENGTH: 301 amino acids  
 ;    TYPE: amino acid  
 ;    STRANDEDNESS: single  
 ;    TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; ORIGINAL SOURCE: Rhodobacter capsulatus  
 ; ORGANISM: Rhodobacter capsulatus  
 ; FEATURE:  
 ;    NAME/KEY: Peptide  
 ;    LOCATION: 1..301  
 ; OTHER INFORMATION: Porin protein

Query Match      41.3%;    Score 52;    DB 5;    Length 301;  
 Best Local Similarity      58.8%;    Pred. No. 3.6;  
 Matches 10;    Conservative 2;    Mismatches 5;    Indels 0;    Gaps 0;

RESULT 3  
 PCT-US95-16126-2  
 ; Query Match      41.3%;    Score 52;    DB 5;    Length 301;  
 ; Best Local Similarity      58.8%;    Pred. No. 3.6;  
 ; Matches 10;    Conservative 2;    Mismatches 5;    Indels 0;    Gaps 0;

Query Match      41.3%;    Score 52;    DB 4;    Length 301;  
 Best Local Similarity      58.8%;    Pred. No. 3.6;  
 Matches 10;    Conservative 2;    Mismatches 5;    Indels 0;    Gaps 0;

RESULT 4  
 US-09-199-637A-405  
 ; Sequence 405, Application US/09199637A  
 ; Patent No. 6355411  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: Ausubel, Frederick  
 ;    APPLICANT: Goodman, Howard M.  
 ;    APPLICANT: Rahme, Laurence G.  
 ;    APPLICANT: Mahajan-Miklos, Shalina  
 ;    APPLICANT: Tan, Man-Wah  
 ;    APPLICANT: Cao, Hui  
 ;    APPLICANT: Drenkard, Eliana  
 ;    APPLICANT: Tsongalis, John  
 ; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID  
 ;    SEQUENCES AND USES THEREOF  
 ;    FILE REFERENCE: 00786/361002  
 ; CURRENT APPLICATION NUMBER: US/09/199, 637A  
 ;    CURRENT FILING DATE: 1998-11-25  
 ;    PRIOR APPLICATION NUMBER: 60/066, 517  
 ;    PRIOR FILING DATE: 1997-11-25  
 ;    NUMBER OF SEQ ID NOS: 437  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ;    SEQ ID NO 405  
 ;    LENGTH: 1.198  
 ;    TYPE: PRT  
 ;    ORGANISM: Pseudomonas aeruginosa

Query Match      37.3%;    Score 47;    DB 4;    Length 1198;  
 Best Local Similarity      52.4%;    Pred. No. 99;  
 Matches 11;    Conservative 2;    Mismatches 4;    Indels 4;    Gaps 1;

Query Match      37.3%;    Score 47;    DB 4;    Length 1198;  
 Best Local Similarity      52.4%;    Pred. No. 99;  
 Matches 11;    Conservative 2;    Mismatches 4;    Indels 4;    Gaps 1;

RESULT 5  
 US-09-199-637A-405  
 ; Sequence 1, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 10/196,136  
CURRENT APPLICATION NUMBER: US/09/252,931A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
SEQ ID NO: 31834  
LENGTH: 425  
TYPE: PRF  
ORGANISM: *Pseudomonas aeruginosa*  
US-09-252-931A-31834

Query Match 36.5%; Score 46; DB 4; Length 425;  
Best Local Similarity 56.2%; Pred. No. 43;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 ERGNDNDISPGDGP 20  
Db 65 EQGRNDNASESTGGGQP 80

## RESULT 6

US-08-341-843B-9

Sequence 9, Application US/08341843B  
Patent No. 5,872,225  
GENERAL INFORMATION:  
APPLICANT: Lemmon, Vance  
TITLE OF INVENTION: A Method for Characterizing the  
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and  
Patent No. 5,872,225

TITLE OF INVENTION: The Nucleotide Sequence  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
SUITE: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
MEDIUM TYPE: Storable  
COMPUTER: Compaq Prolinea 5100e  
OPERATING SYSTEM: DOS 5.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/341,843B  
FILING DATE: No. 5872225ember 18, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/904,991  
FILING DATE: June 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Minnich, Richard J.

REGISTRATION NUMBER: 24,175

REFERENCE/DOCKET NUMBER: CWR 2 149-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (216) 611-5582

TELEFAX: (216) 241-1666

TELEX: (216) 980162

SEQUENCE CHARACTERISTICS:

LENGTH: 96

TYPE: amino acid

STRAND/DNESS: single

TOPOLOGY: linear

## RESULT 7

US-08-341-843B-9

Sequence 14, Application US/08427497E

Patent No. 5,963,124

GENERAL INFORMATION:

APPLICANT: Lemmon, Vance

TITLE OF INVENTION: A Method for Characterizing the

TITLE OF INVENTION: Nucleotide Sequence of L1CAM and

Patent No. 5,963,124

TITLE OF INVENTION: the Nucleotide Sequence

TITLE OF INVENTION: Characterized Thereby

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich &amp; McKee

STREET: 1100 Superior Avenue

SUITE: Suite 700

CITY: Cleveland

STATE: Ohio

COUNTRY: U.S.A.

ZIP: 44114-2518

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

MEDIUM TYPE: Storable

COMPUTER: Compaq Prolinea 5100e

OPERATING SYSTEM: DOS 5.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/341,843B

FILING DATE: No. 5872225ember 18, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/904,991

FILING DATE: June 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Minnich, Richard J.

REGISTRATION NUMBER: 24,175

REFERENCE/DOCKET NUMBER: CWR 2 149-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (216) 611-5582

TELEFAX: (216) 241-1666

TELEX: (216) 980162

SEQUENCE CHARACTERISTICS:

LENGTH: 96

TYPE: amino acid

STRAND/DNESS: single

TOPOLOGY: linear

MOLECULE TYPE: amino acids  
HYPOTHETICAL: irrelevant  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: mouse  
INDIVIDUAL ISOLATE: 8 day old mouse brain  
IMMEDIATE SOURCE:  
LIBRARY: lambda GT 10 and lambda GT11  
CLONE: synthesis of several clones  
PUBLICATION INFORMATION:  
AUTHORS: Moos, M.  
AUTHORS: Tacke, R.  
AUTHORS: Scherer, H.  
AUTHORS: Teplow, D.  
AUTHORS: Frun, K.  
AUTHORS: Schachner, M.  
TITLE: Neural adhesion molecule L1 is a member of the immunoglobulin superfamily with binding domains similar to fibronectin  
JOURNAL: NATURE  
VOLUME: 334  
ISSUE: 701-703  
PAGES: 701-703  
DATE: 1988  
US-08-341-843B-9

Query Match 36.1%; Score 45.5%; DB 2; Length 96;  
Best Local Similarity 61.1%; Pred. No. 9.4;  
Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 2 DIQERGDNDISPGDQ 19  
Db 41 DIQERGSD-KYFIELDGK 57

RESULT 7  
US-08-427-497E-14  
Sequence 14, Application US/08427497E  
Patent No. 5,963,124  
GENERAL INFORMATION:  
APPLICANT: Lemmon, Vance  
TITLE OF INVENTION: A Method for Characterizing the  
TITLE OF INVENTION: Nucleotide Sequence of L1CAM and  
Patent No. 5,963,124  
TITLE OF INVENTION: the Nucleotide Sequence  
TITLE OF INVENTION: Characterized Thereby  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
SUITE: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
TITLE OF INVENTION: Characterized Thereby  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay, Sharpe, Beall, Fagan,  
ADDRESSEE: Minnich & McKee  
STREET: 1100 Superior Avenue  
SUITE: Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: U.S.A.  
ZIP: 44114-2518  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
MEDIUM TYPE: Storable  
COMPUTER: Compaq Prolinea 5100e  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/347,497E  
FILING DATE: April 24, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/904,991  
FILING DATE: June 26, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Minnich, Richard J.  
REGISTRATION NUMBER: 24,175

REFERENCE/DOCKET NUMBER: CWR 2 149-3-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (216) 861-5582

TELEFAX: (216) 241-1666

TELEX: (216) 980162

SEQUENCE CHARACTERISTICS: 14:

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: amino acids

HYPOTHETICAL: irrelevant

ANTI-SENSE: no

ORIGINAL SOURCE:

ORGANISM: mouse

INDIVIDUAL ISOLATE: 8 day old mouse brain

IMMEDIATE SOURCE:

LIBRARY: lamda GT 10 and lamda GT11

CLOSE: synthesis of several clones

PUBLICATION INFORMATION:

AUTHORS: Moos, M.

AUTHORS: Tacke, R.

AUTHORS: Scherer, H.

AUTHORS: Teplow, D.

AUTHORS: Fruh, K.

AUTHORS: Schachner, M.

TITLE: Neural adhesion molecule L1 is a

TITLE: member of the immunoglobulin

TITLE: superfamily with binding domains

TITLE: similar to fibronectin

JOURNAL: NATURE

VOLUME: 334

ISSUE:

PAGES: 701-703

DATE: 1988

US-08-427-497E-14

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.4;

Length 96;

Score 45.5; DB 2;

Length 96;

Indels 1;

Gaps 1;

Matches 11;

Conservative 2;

Mismatches 4;

DB

2 DLQERGNDNPFSFGDQ 19

41 DLQERGDS-D-KYFIELDGK 57

Query Match

Best Local Similarity 36.1%;

Pred. No. 1.8e+02;

Length 1260;

Score 45.5; DB 4;

Length 1260;

Indels 4;

Gaps 1;

Matches 11;

Conservative 2;

Mismatches 4;

DB

2 DLQERGNDNPFSFGDQ 19

558 DLQERGDS-D-KYFIELDGK 574

RESULT 8

US-09-252-991A-22899

Sequence 22899, Application US/09252991A

Patent No. 655175

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22899

LENGTH: 101

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22899

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Sequence 32044, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: 107196,116

FILE REFERENCE: 107196,116

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-07-27

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

TYPE: PRF

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32044

Query Match

Best Local Similarity 36.1%;

Pred. No. 9.9;

Length 101;

Mismatches 3;

Indels 7;

Gaps 1;

Matches 9;

Conservative 42.9%;

Prior Filing Date: 1998-07-27

Number of Seq Id Nos: 33142

Seq Id No 32044

Length: 101

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LENGTH: 547
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32044

Query Match      35.7% Score 45; DB 4; Length 547;
Best Local Similarity 38.5%; Pred. No. 81;
Matches 10; Conservative 5; Mismatches 7; Indels 4; Gaps 1;
US-08-176-126B-2

Qy      2 DLOERGNDNDISPPSGD---GQPFKD 23
Db      411 EADEVGGDDLVPGAGNROELGQPLHD 436

RESULT 11
US-09-328-352-7703
Sequence 7703, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCUSIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUmannii FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03 PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7703

Length: 186
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7703

Query Match      34.9% Score 44; DB 4; Length 186;
Best Local Similarity 38.1%; Pred. No. 33;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
US-08-176-126B-2

Qy      3 LOERGNDNDISPPSGDGPFFKD 23
Db      73 LETHGETDPSFVSELYEHD 93

RESULT 12
US-08-176-126B-2
Sequence 2, Application US/08176126B
Patent No. 5589358

GENERAL INFORMATION:
APPLICANT: Dawson, Paul A.
TITLE OF INVENTION: ILEAL BILE ACID TRANSPORTER COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,435
FILING DATE: 26-JUN-1996
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/176,126
FILING DATE: 29-DEC-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: WAKE:002/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: na
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-669-435-2

Query Match      34.9% Score 44; DB 2; Length 348;
Best Local Similarity 53.3%; Pred. No. 68;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
US-08-176-126B-2

Qy      1 TDLOERGNDNDISPPS 15
Db      320 TELQEKTDNEMEPRS 334

RESULT 14

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PCT-US94-14431A-2  
 Sequence 2 Application PC/TUSS9414431A  
 GENERAL INFORMATION:  
 APPLICANT: TITLE: ILEAL BILE ACID TRANSPORTER COMPOSITIONS  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P. O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
 SOFTWARE: PatentIn Release #1.0, Version  
 SOFTWARE: #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/14431A  
 FILING DATE: 29-DEC-1994  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/176,126  
 FILING DATE: 29-DEC-1993  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARKER, DAVID L.  
 REGISTRATION NUMBER: 32,165  
 REFERENCE/DOCKET NUMBER: WAKE005P--  
 TELEPHONE: (512) 418-3000  
 TELEX: (713) 789-2679  
 TELEX: 79-0924(1) GENERAL INFORMATION:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 348 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US94-14431A-2

Query Match 34.9%; Score 44; DB 5; Length 348;  
 Best Local Similarity 53.3%; Pred. No. 68; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TDLOERGNDNDISPPFS 15  
 Db 320 TELQETKDNEMEPR 334

RESULT 15  
 US-08-278-091-6  
 Sequence 6, Application US/08278091  
 Patient No. 5506139  
 GENERAL INFORMATION:  
 APPLICANT: LOOSMORE, Sheena M  
 APPLICANT: YANG, Yan-Ping  
 APPLICANT: CHONG, Pele  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: KUBIN, Michel H.  
 TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Activity  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7  
 COMPUTER READABLE FORM:

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model.

Run on: January 29, 2004, 12:38:39 ; Search time 32.6842 Seconds

(without alignments)

146.247 Million cell updates/sec

Title: US-09-812-485A-49

Perfect score: 126

Sequence: 1 TDLOERGNDNDISPPFGQPFKD 23

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207024079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡

Maximum Match 100§

Listing first 45 summaries

Database : Published\_Applications\_AA:<sup>\*</sup>

1: /cn2\_6\_ptodata/1/pubbaa/US07\_PUBCOMB.pep:\*

2: /cn2\_6\_ptodata/1/pubbaa/US07\_PUBCOMB.pep:\*

3: /cn2\_6\_ptodata/1/pubbaa/US07\_NET\_PUB.pep:\*

4: /cn2\_6\_ptodata/1/pubbaa/US07\_PUBCOMB.pep:\*

5: /cn2\_6\_ptodata/1/pubbaa/US08\_PUB.pep:\*

6: /cn2\_6\_ptodata/1/pubbaa/US08\_PUBCOMB.pep:\*

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10: /cn2\_6\_ptodata/1/pubbaa/US09B\_PUBCOMB.pep:\*

11: /cn2\_6\_ptodata/1/pubbaa/US09C\_PUBCOMB.pep:\*

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14: /cn2\_6\_ptodata/1/pubbaa/US10B\_PUBCOMB.pep:\*

15: /cn2\_6\_ptodata/1/pubbaa/US10C\_PUBCOMB.pep:\*

16: /cn2\_6\_ptodata/1/pubbaa/US60\_NEW\_PUB.pep:\*

17: /cn2\_6\_ptodata/1/pubbaa/US60\_NET\_PUB.pep:\*

18: /cn2\_6\_ptodata/1/pubbaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match length DB ID Description

Result No.	Score	Query Match length	DB ID	Description
1	126	100.0	23	10 US-09-812-485A-49
2	126	100.0	23	12 US-10-360-202-1
3	126	100.0	24	12 US-10-360-202-17
4	126	100.0	24	12 US-10-360-202-18
5	126	100.0	97	10 US-09-812-485A-1
6	126	100.0	509	12 US-09-794-422-34
7	126	100.0	525	10 US-09-814-550-2
8	126	100.0	525	12 US-09-794-422-6
9	126	100.0	525	12 US-10-311-840-1
10	126	100.0	540	12 US-09-794-422-46
11	126	100.0	556	12 US-09-794-422-8
12	123	97.6	23	12 US-10-360-202-4
13	115	91.3	21	12 US-10-360-202-6
14	112	88.9	23	12 US-10-360-202-2
15	110	87.3	20	12 US-10-360-202-8

SEQ ID NO: 49

LENGTH: 23

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: D-00006 peptide  
NAME/KEY: AMIDATION  
LOCATION: 15  
US-09-812-485A-49

RESULT 1  
US-09-812-485A-49  
; Sequence 49, Application US/09812485A  
; Publication No. US20020197267A1  
; GENERAL INFORMATION:  
; APPLICANT: Kumagai, Yoshinari  
; Blacher, Rusele  
; Yoneda, Toshiyuki  
; TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases  
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases  
; FILE REFERENCE: BEAR-006CIP  
; CURRENT APPLICATION NUMBER: US/09/812, 485A  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09-641,034  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ For Windows Version 4.0

RESULT 2  
US-10-360-202-1

Sequence 11, App1  
Sequence 9, App1  
Sequence 3, App1  
Sequence 7, App1  
Sequence 12, App1  
Sequence 21, App1  
Sequence 13, App1  
Sequence 6, App1  
Sequence 48, App1  
Sequence 30, App1  
Sequence 47, App1  
Sequence 10, App1  
Sequence 5, App1  
Sequence 2, App1  
Sequence 4, App1  
Sequence 16, App1  
Sequence 14, App1  
Sequence 46, App1  
Sequence 24, App1  
Sequence 32, App1  
Sequence 26, App1  
Sequence 25, App1  
Sequence 17, App1  
Sequence 12, App1  
Sequence 10, App1  
Sequence 8, App1  
Sequence 5, App1  
Sequence 4959, App1

#### ALIGNMENTS

RESULT 1  
US-09-812-485A-49  
; Sequence 49, Application US/09812485A  
; Publication No. US20020197267A1  
; GENERAL INFORMATION:  
; APPLICANT: Kumagai, Yoshinari  
; Blacher, Rusele  
; Yoneda, Toshiyuki  
; TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases  
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases  
; FILE REFERENCE: BEAR-006CIP  
; CURRENT APPLICATION NUMBER: US/09/812, 485A  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09-641,034  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ For Windows Version 4.0

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-12;

Mismatches 0; Conservative 0; Gaps 0;

SEQ ID NO: 49

LENGTH: 23

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: D-00006 peptide  
NAME/KEY: AMIDATION  
LOCATION: 15  
US-09-812-485A-49  
Qy |||||  
Db |||||  
1 TDLOERGNDNDISPPFGQPFKD 23  
1 TDLOERGNDNDISPPFGQPFKD 23

Sequence 1, Application US/10360202  
; GENERAL INFORMATION: US20030186891A1  
; APPLICANT: Okano, Toshio  
; APPLICANT: Nakagawa, Naoko  
; APPLICANT: Nakagawa, Kimie  
; APPLICANT: Blacher, Russell W  
; APPLICANT: Kumagai, Yoshinari  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
; TITLE OF INVENTION: OF VITAMIN D DEFICIENCY  
; FILE REFERENCE: BEAR-010  
; CURRENT APPLICATION NUMBER: US/10/360,202  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,548  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO: 1  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligopeptide  
US-10-360-202-1

Query Match	100.0%	Score 126;	DB 12;	Length 23;
Best Local Similarity	100.0%	Pred. No. 1.6e-12;		
Matches	23;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1	TDLQERGNDNDISPFSGDQGPFKD	23	
Db	1	TDLQERGNDNDISPFSGDQGPFKD	23	

RESULT 3  
US-10-360-202-17  
; Sequence 17, Application US/10360202  
; GENERAL INFORMATION: US20030186891A1  
; APPLICANT: Okano, Toshio  
; APPLICANT: Nakagawa, Naoko  
; APPLICANT: Nakagawa, Kimie  
; APPLICANT: Blacher, Russell W  
; APPLICANT: Kumagai, Yoshinari  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT  
; TITLE OF INVENTION: OF VITAMIN D DEFICIENCY  
; FILE REFERENCE: BEAR-010  
; CURRENT APPLICATION NUMBER: US/10/360,202  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,548  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligopeptide  
US-10-360-202-17

Query Match	100.0%	Score 126;	DB 12;	Length 24;
Best Local Similarity	100.0%	Pred. No. 1.6e-12;		
Matches	23;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1	TDLQERGNDNDISPFSGDQGPFKD	23	
Db	2	TDLQERGNDNDISPFSGDQGPFKD	24	

RESULT 4  
US-10-360-202-18  
; Sequence 18, Application US/10360202

RESULT 5  
US-09-812-485A-1  
; Sequence 1, Application US/09812485A  
; Publication No. US20020197267A1  
; GENERAL INFORMATION:  
; APPLICANT: Blacher, Russell  
; APPLICANT: Yoneda, Toshiyuki  
; APPLICANT: Kumagai, Yoshinari  
; TITLE OF INVENTION: Integrin Binding Motif Containing Skeletal Diseases  
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases  
; FILE REFERENCE: BEAR-00CCP  
; CURRENT APPLICATION NUMBER: US/09/812,485A  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/641,034  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptidic compound  
US-09-812-485A-1

Query Match	100.0%	Score 126;	DB 10;	Length 97;
Best Local Similarity	100.0%	Pred. No. 8.1e-12;		
Matches	23;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1	TDLQERGNDNDISPFSGDQGPFKD	23	
Db	43	TDLQERGNDNDISPFSGDQGPFKD	65	

RESULT 6  
US-09-794-422-34  
; Sequence 34, Application US/09794422  
; Publication No. US20030166239A1  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Thomas A.

```

; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIORITY NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIORITY NUMBER: 60/234,500
; PRIORITY NUMBER: 60/234,500
; PRIORITY NUMBER: 60/234,500
; PRIORITY NUMBER: 60/234,500
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 34
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-794-422-34

Query Match 100.0%; Score 126; DB 12; Length 509;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 226 TDLQERGNDISPGSGDQPFKD 248
Db 226 TDLQERGNDISPGSGDQPFKD 248

RESULT 7
US-09-814-550-2
; Sequence 2, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
; FILE REFERENCE: 5014.US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIORITY NUMBER: US 60/181,786
; PRIOR FILING DATE: 2000-03-24
; PRIORITY NUMBER: US 60/241,598
; PRIORITY NUMBER: US 60/241,598
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO: 2
; LENGTH: 525
; SOFTWARE: PatentIn version 3.0
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-814-550-2

Query Match 100.0%; Score 126; DB 10; Length 525;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 242 TDLQERGNDISPGSGDQPFKD 264
Db 242 TDLQERGNDISPGSGDQPFKD 264

RESULT 8
US-09-794-422-6
; Sequence 6, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIORITY NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIORITY NUMBER: 60/234,500
; PRIORITY NUMBER: 60/234,500
; PRIORITY NUMBER: 60/234,500
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-794-422-6

Query Match 100.0%; Score 126; DB 12; Length 525;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 242 TDLQERGNDISPGSGDQPFKD 264
Db 242 TDLQERGNDISPGSGDQPFKD 264

RESULT 9
US-10-311-840-1
; Sequence 1, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto
; TITLE OF INVENTION: No. US20030175808A1 Protein and its DNA
; FILE REFERENCE: 2738US0P
; CURRENT APPLICATION NUMBER: US/10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIORITY NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIORITY NUMBER: JP 2000-191088
; PRIORITY NUMBER: JP 2000-191088
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO: 1
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Human
; US-10-311-840-1

Query Match 100.0%; Score 126; DB 12; Length 525;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 242 TDLQERGNDISPGSGDQPFKD 264
Db 242 TDLQERGNDISPGSGDQPFKD 264

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; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 46
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-46

Query Match          100.0%; Score 126; DB 12; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 TDLQERGNDNTSPFSGDGGOPFKD 23
Db    257 TDLQERGNDNTSPFSGDGGOPFKD 279

RESULT 11
US-09-794-422-8
; Sequence 8 Application US/09794422
; Publication No. US2003166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/155,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-8

Query Match          100.0%; Score 126; DB 12; Length 556;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 TDLQERGNDNTSPFSGDGGOPFKD 23
Db    273 TDLQERGNDNTSPFSGDGGOPFKD 295

RESULT 12
US-10-360-202-4
; Sequence 4 Application US/103600202
; Publication No. US2003186891A1
; GENERAL INFORMATION:
; APPLICANT: Okano, Toshio
; APPLICANT: Tsugawa, Naoko
; APPLICANT: Nakagawa, Kimie
; APPLICANT: Blacher, Russell W
; APPLICANT: Kumagai, Yoshinari
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; FILE REFERENCE: BEAR-010
; CURRENT APPLICATION NUMBER: US/10/360,202
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,548
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial sequence
US-10-360-202-4

Query Match          97.6%; Score 123; DB 12; Length 23;
Best Local Similarity 95.7%; Pred. No. 4.6e-12;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy   1 TDLOQERGNDNDSPFGDQOPFKD 23
Db    1 TDLOQERGNDNDSPFGDQOPFKD 23

RESULT 13
US-10-360-202-6
; Sequence 6 Application US/10360202
; Publication No. US2003186891A1
; GENERAL INFORMATION:
; APPLICANT: Okano, Toshio
; APPLICANT: Tsugawa, Naoko
; APPLICANT: Nakagawa, Kimie
; APPLICANT: Blacher, Russell W
; APPLICANT: Kumagai, Yoshinari
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; FILE REFERENCE: BEAR-010
; CURRENT APPLICATION NUMBER: US/10/360,202
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,548
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide
US-10-360-202-6

Query Match          91.3%; Score 115; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 TDLOQERGNDNDSPFGDQOPF 21
Db    1 TDLOQERGNDNDSPFGDQOPF 21

RESULT 14
US-10-360-202-2
; Sequence 2 Application US/10360202
; Publication No. US2003186891A1
; GENERAL INFORMATION:
; APPLICANT: Okano, Toshio
; APPLICANT: Tsugawa, Naoko
; APPLICANT: Nakagawa, Kimie
; APPLICANT: Blacher, Russell W
; APPLICANT: Kumagai, Yoshinari
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; FILE REFERENCE: BEAR-010
; CURRENT APPLICATION NUMBER: US/10/360,202
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,548
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial sequence
US-10-360-202-2

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; FEATURE:
; OTHER INFORMATION: Synthetic oligopeptide
US-10-360-204-2

Query Match          88.9%; Score 112; DB 12; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.e-10;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TDLOERGNDNDISPPSGDGGPFDK 23
Db      1 DLQERGNDNDISPPSGDGGPFDK 23

RESULT 15
US-10-360-202-8

Sequence 8 Application US/1060202
Publication No. US20030186891A1

GENERAL INFORMATION:
; APPLICANT: Okano, Toshiro
; APPLICANT: Tsugawa, Naoko
; APPLICANT: Nakagawa, Kimie
; APPLICANT: Blacher, Russell W
; APPLICANT: Kumagai, Yoshinari
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: OF VITAMIN D DEFICIENCY
; FILE REFERENCE: BEAR-010
; CURRENT APPLICATION NUMBER: US/10/360,202
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,548
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic oligopeptide
US-10-360-204-8

Query Match          87.3%; Score 110; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DLQERGNDNDISPPSGDGGP 21
Db      1 DLQERGNDNDISPPSGDGGP 20

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2	52	41.3	320	JC5727	porin - Rhodobacter capsulatus porin precursor - Rhodobacter capsulatus porin precursor - Rhodobacter capsulatus
3	49.5	39.3	1259	S36126	lyszyme (EC 3.2.1.48)
4	48	38.1	277	AD3322	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
5	48	38.1	385	D72858	lyszyme (EC 3.2.1.48)
6	48	38.1	385	T41811	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
7	47	37.3	444	B83891	lyszyme (EC 3.2.1.48)
8	47	37.3	481	AH0410	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
9	47	37.3	825	B89944	lyszyme (EC 3.2.1.48)
10	46.5	36.9	1106	S378783	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
11	46.5	36.9	1135	I61186	lyszyme (EC 3.2.1.48)
12	46.5	36.9	1137	JCS950	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
13	46	36.5	308	AD3154	lyszyme (EC 3.2.1.48)
14	46	36.5	365	E98133	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
15	45.5	36.1	347	A81170	lyszyme (EC 3.2.1.48)
16	45.5	36.1	1260	S05479	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
17	45	35.7	158	AI1365	lyszyme (EC 3.2.1.48)
18	45	35.7	357	C84856	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
19	45	35.7	393	S59499	lyszyme (EC 3.2.1.48)
20	45	35.7	472	JQ0802	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
21	45	35.7	851	T38175	lyszyme (EC 3.2.1.48)
22	45	35.7	913	D82885	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
23	44.5	35.3	698	D65210	lyszyme (EC 3.2.1.48)
24	44.5	35.3	698	D91255	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
25	44.5	35.3	698	H86095	lyszyme (EC 3.2.1.48)
26	44	34.9	348	A49876	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
27	44	34.9	475	S15337	lyszyme (EC 3.2.1.48)
28	44	34.9	475	AC0528	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
29	44	34.9	683	D83511	lyszyme (EC 3.2.1.48)

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OM protein - protein search, using SW model

Run on: January 29, 2004, 12:36:28 ; Search time 16:34:21 Seconds (without alignments)

Total: US-09-812-485A-49

Perfect score: 126

Sequence: 1 TDLOERGNDNDISPPFGDGGPKD 23

Scoring table: BL05308 seqs, 96168682 residues

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\* Maximum Match 100\*

Listing first 45 summaries

Database : PIR\_76.1\*

1: PIR1;\*

2: PIR2;\*

3: PIR3;\*

4: PIR4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	41.3	301	S16070	porin - Rhodobacter capsulatus porin precursor - neural cell adhesion molecule (EC 3.2.1.48) lyszyme (EC 3.2.1.48) late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
2	52	41.3	320	JC5727	porin - Rhodobacter capsulatus porin precursor - Rhodobacter capsulatus porin precursor - Rhodobacter capsulatus
3	49.5	39.3	1259	S36126	lyszyme (EC 3.2.1.48)
4	48	38.1	277	AD3322	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
5	48	38.1	385	D72858	lyszyme (EC 3.2.1.48)
6	48	38.1	385	T41811	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
7	47	37.3	444	B83891	lyszyme (EC 3.2.1.48)
8	47	37.3	481	AH0410	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
9	47	37.3	825	B89944	lyszyme (EC 3.2.1.48)
10	46.5	36.9	1106	S378783	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
11	46.5	36.9	1135	I61186	lyszyme (EC 3.2.1.48)
12	46.5	36.9	1137	JCS950	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
13	46	36.5	308	AD3154	lyszyme (EC 3.2.1.48)
14	46	36.5	365	E98133	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
15	45.5	36.1	347	A81170	lyszyme (EC 3.2.1.48)
16	45.5	36.1	1260	S05479	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
17	45	35.7	158	AI1365	lyszyme (EC 3.2.1.48)
18	45	35.7	357	C84856	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
19	45	35.7	393	S59499	lyszyme (EC 3.2.1.48)
20	45	35.7	472	JQ0802	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
21	45	35.7	851	T38175	lyszyme (EC 3.2.1.48)
22	45	35.7	913	D82885	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
23	44.5	35.3	698	D65210	lyszyme (EC 3.2.1.48)
24	44.5	35.3	698	D91255	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
25	44.5	35.3	698	H86095	lyszyme (EC 3.2.1.48)
26	44	34.9	348	A49876	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
27	44	34.9	475	S15337	lyszyme (EC 3.2.1.48)
28	44	34.9	475	AC0528	late expression fa LEPF3 orf67 - Bomb intracellular alka global stress regul hypothesis protein integrin alpha-7 integrin - integrin alpha-7 C nucleotidyltransferase hypothesis protein S-adenylylmonophosphate (EC 2.7.7.4) neural cell adhesion protein a probable repressor protein k cellulase egII - S levansucrase (EC 2.4.1.11) multiple bands on SDS-PAGE ybbH protein precursor hypothesis protein Na+ dependent bile heat shock protein precursor DO precursor flagellar hook-asso
29	44	34.9	683	D83511	lyszyme (EC 3.2.1.48)

ALIGMENTS

RESULT 1

S16070

porin - Rhodobacter capsulatus

C:Species: Rhodobacter capsulatus

C:Date: 21-Nov-1993 #sequence\_revision 21-Jul-1995

C:Accession: S16070

R.Schultz, B.; Kreusch, A.; Nestel, U.; Schulz, G.E.

Eur. J. Biochem. 199, 587-594, 1991

A:Title: Primary structure of porin from Rhodobacter capsulatus.

A:Reference number: S16070; PMID:1651239

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-301 <EUR>

A:Experimental source: strain 37B4

A:Note: the source is designated as Rhodobacter capsulatus

Query Match 41.3\*; Score 52; DB 2; Length 301;

Best Local Similarity 58.8\*; Pred. No. 3.1; Mismatches 10; Conservative 10; Matches 10; Gapless 0; Gaps 0;

Query 1 TDLQERGNDNDISPFSGD 17

Db 92 TDUDRGNDNPILYGD 108

RESULT 2

JCS727

porin precursor - Rhodobacter capsulatus

C:Species: Rhodobacter capsulatus

C:Accession: JC5727; PC4414

R.Trieschmann, M.D.A.; Pattus, F.; Tadros, M.H.

Gene 103, 61-68, 1996

A:Title: Molecular characterization and organization of porin from Rhodobacter capsulatus

A:Reference number: JC5727; PMID:9749280; PMID:8936088

A:Accession: JC5727

A:Molecule type: protein

A:Residues: 1-320 <TRI>

A:Cross references: GB:U57653

A:Experimental source: strain 37B4

A:Accession: PC4414

A:Gene: PorCa

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-320/Product: porin #status predicted <MAT>

Query Match 41.3\*; Score 52; DB 2; Length 320;

Best Local Similarity 58.8%; Pred. No. 3.3;  
Matches 10; Conservative 2; Mismatches 5;  
Indels 0; Gaps 0;

Qy 1 TDLOERGNDNDISPFSGD 17  
Db 112 TDLDGRGGNDIPYLTD 128

**RESULT 3**

S36126 neural cell adhesion molecule L1 - rat  
neuronal names: nerve growth factor-inducible large external glycoprotein; NILE glyco-  
C; Species: Rattus norvegicus (Norway rat)  
C; Date: 13-Jan-1995 #text\_change 20-Aug-1999  
C; Accession: S36126; S17655; A60917; A30326  
R.; Miura, M.; Kobayashi, M.; Asou, H.; Uyemura, K.  
FEBS Lett. 289, 91-95, 1991  
A; Title: Molecular cloning of cDNA encoding the rat neural cell adhesion molecule L1. Tw-  
A; Reference number: S17655; MUID:91372414; PMID:1894411  
A; Accession: S36126  
A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-1259 <MIU>  
A; Cross-references: EMBL: X59149  
A; Accession: S17655  
A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-1178-1183-1259 <MI2>  
R.; Prince, J.T.; Milona, N.; Stallcup, W.B.  
J. Neurosci. 9, 1829-1834, 1989  
A; Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identifi-  
A; Reference number: A60917; MUID:9225727; PMID:2723751  
A; Accession: A60917  
A; Status: not compared with conceptual translation  
A; Molecule type: mRNA  
A; Residues: 1159-1199'G', 1201-1215,'K',1237 <PRI>  
A; Reference number: A30326; MUID:89177485; PMID:2466366  
A; Note: this paper appeared earlier, with printing errors, as reference A30326  
R.; Prince, J.T.; Milona, N.; Stallcup, W.B.  
J. Neurosci. 9, 876-883, 1989  
A; Title: Characterization of a partial cDNA clone for the NILE glycoprotein and identifi-  
A; Reference number: A30326; MUID:89177485; PMID:2466366  
A; Contents: annotation  
A; Note: this paper was reprinted as reference A60917 to correct the omission of several  
C; Comment: This sequence of this surface-accessible glycoprotein differs at only two pos-  
accessible only after treatment of cells with detergent and is assumed to be cytoplasmic  
C; Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; 1  
C; Keywords: cell adhesion; duplication; glycoprotein; membrane protein  
F; 531-592/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 49.5%; DB 2; Length 1259;  
Best Local Similarity 66.7%; Pred. No. 37;  
Matches 12; Conservative 1; Mismatches 4;  
Indels 1; Gaps 1;

Qy 2 DLQERGNDNDISPFSGDQ 19  
Db 558 DLQERGNDSD-KYFIEDQ 574

**RESULT 4**

AD3122 Lysozyme (EC 3.2.1.17) - Brucella melitensis (strain 16M)  
C; Species: Brucella melitensis  
C; Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 19-Apr-2002  
R.; DeVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier,  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A; Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A; Reference number: AD3252; PMID:11756688  
A; Accession: AD3322  
A; Status: preliminary  
A; Molecule type: DNA

Query Match 38.1%; Score 48%; DB 2; Length 277;  
Best Local Similarity 52.9%; Pred. No. 11;  
Matches 9; Conservative 3; Mismatches 5;  
Indels 0; Gaps 0;

Qy 6 RGDNNDISPFSGDQPFK 22  
Db 252 RGDDADNTFGDASWK 268

**RESULT 5**

D72858 late expression factor 3 - Autographa californica nuclear polyhedrosis virus  
C; Species: Autographa californica nuclear polyhedrosis virus, AcMNPV  
A; Note: dsDNA virus  
C; Accession: D72858; A40677  
C; Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 24-Nov-1999  
C; Accession: D72858; A40677  
R.; Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.  
Virology 202, 586-605, 1994  
A; Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.  
A; Reference number: A72850; MUID:94303173; PMID:8030224  
A; Accession: D72858  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-385 <AYR>  
A; Cross-references: GB:L22858; NID:9510708; PMID:AAA66697.1; PID:9559136  
R.; Li, Y.; Passarelli, A.L.; Miller, L.K.  
J. Virol. 67, 5260-5268, 1993  
A; Title: Identification, sequence, and transcriptional mapping of lef-3, a baculovirus 96  
A; Reference number: A40677; MUID:93353600; PMID:8350397  
A; Accession: A40677  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-385 <LYA>  
A; Cross-references: GB:L18873; NID:9349019; PMID:AAA02964.1; PID:9349020  
A; Note: authors translated the codon ACA for residue 92 as Tyr  
C; Genes:  
A; Gene: Ac-lef3  
C; Keywords: transcription regulation

Query Match 38.1%; Score 48%; DB 2; Length 385;  
Best Local Similarity 56.2%; Pred. No. 17;  
Matches 9; Conservative 1; Mismatches 6;  
Indels 0; Gaps 0;

Qy 8 DNDISPFSGDQPFK 23  
Db 61 DNKIQEYGDQSFKD 76

**RESULT 6**

T41811 LEP-3 orf67 - Bombyx mori nuclear polyhedrosis virus (isolate T3)  
C; Species: Bombyx mori nuclear polyhedrosis virus, BmSNPv  
A; Variety: isolate T3  
C; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C; Accession: T41811  
R.; Gomi, S.; Majima, K.; Maeda, S.  
J. Gen. Virol. 80, 1223-1337, 1999  
A; Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.  
A; Reference number: 222020; MUID:10155780  
A; Accession: T41811  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-385 <KAM>  
A; Cross-references: ENBL:L33180; NID:93745835; PMID:AAC63740.1; PID:93745893  
A; Experimental source: isolate T3

C;Genetics:  
A;Note: lef-3

Query Match 38.1%; Score 48; DB 2; Length 385;  
Best Local Similarity 56.2%; Pred. No. 17;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 8 DNDISPFGDQPFKD 23  
Db 61 DNKIQEYFGDSQSFKD 76

RESULT 7

B83891

Intracellular alkaline serine proteinase aprx [imported] - *Bacillus halodurans* (strain C)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001

C;Accession: B83891

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A;Reference number: AB3650; MUID:11058132

A;Accession: B83891

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-444 <STO>

A;Cross-references: GB:AP001513; GB:BA000004; NID:910174345; PIDN:BAB05649.1; GSPDB:GN00

C;Genetics:  
A;Gene: aprx

Query Match 37.3%; Score 47; DB 2; Length 444;

Best Local Similarity 47.1%; Pred. No. 28;

Mismatches 4; Indels 0; Gaps 0;

Qy 2 DLOERGDNNDISPFGDG 18  
Db 319 DTDRDDDVAPFSSRG 335

RESULT 8

AH0410

9100 stress requirement protein GsrA [imported] - *Yersinia pestis* (strain C992)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 17-May-2002

C;Accession: AH0410

R;Parikhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skeilton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001

A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0410

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-481 <KUR>

A;Cross-references: GB:AL590842; PIDN:CA92612.1; PID:g15981308; GSPDB:GN00175

C;Genetics:  
A;Gene: GsrA

C;Superfamily: Helicobacter serine proteinase

Query Match 37.3%; Score 47; DB 2; Length 481;

Best Local Similarity 62.5%; Pred. No. 30;

Mismatches 1; Indels 2; Gaps 1;

Qy 7 GNDISPFSGDQPFK 22  
Db 80 GDN-SPPFDQDGSFQ 93

RESULT 9

B8944

hypothetical protein SAl447 [imported] - *Staphylococcus aureus* (strain N315)

C;Species: *Staphylococcus aureus*

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001

C;Accession: B8944

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.

A;Reference number: A89758; MUID:23311952; PMID:1418146

A;Accession: B8944

A;Molecule type: DNA

A;Status: preliminary

A;Cross-references: GB:BA000018; PID:g13701417; PIDN:BAB42711.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:  
A;Gene: SAl447

C;Generic:

A;Accession: SAl447

A;Molecule type: DNA

A;Status: preliminary

A;Cross-references: <KUR>

A;Experimental source: strain N315

C;Species: *Staphylococcus aureus*

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001

C;Accession: B8944

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.

A;Reference number: A89758; MUID:23311952; PMID:1418146

A;Accession: B8944

A;Molecule type: DNA

A;Status: preliminary

A;Cross-references: <KUR>

A;Experimental source: strain N315

C;Genetics:  
A;Gene: SAl447

C;Generic:

A;Accession: SAl447

A;Molecule type: DNA

A;Status: preliminary

A;Cross-references: <KUR>

A;Experimental source: strain N315

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 22-Jan-1994 #sequence\_revision 14-Jul-1995 #text\_change 29-Sep-1999

C;Accession: S23600

R;Kaufman, S.J.

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: EMBL:X65036; NID:956192; PIDN:CAA46170.1; PID:956193

R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S22600

A;Accession: S22600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: EMBL:X65036

C;Superfamily: integrin alpha/beta chain

A;Accession: S215319

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;Cross-references: <KRAU>

A;Experimental source: R;Song, W.K.; Wang, W.; Foster, R.F.; Biebler, D.A.; Kaufman, S.J.

J;Cell Biol. 117, 613-617, 1992

A;Title: H36-alphA7 is a novel integrin alpha chain that is developmentally regulated during embryonic development

A;Reference number: S23600

A;Accession: S23600

A;Molecule type: mRNA

A;Status: preliminary

A;

A; Molecule type: mRNA  
A; Residues: 1-1135 <RES>  
C; Cross-references: GB:L23423; NID:9431415; PIDN:AAA16600.1; PMID:9431416  
C; Superfamily: integrin alpha-2b chain

Query Match Score 46.5; DB 2; Length 1135;  
Best Local Similarity 47.8%; Pred. No. 94; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 2 DLQERGDNF---SPFSGCQPF 21  
Db 390 DLNQDGFPDIAGAPFDGDSKVF 412

---

RESULT 12

JC950 integrin alpha-7 chain precursor - human  
C; Species: Homo sapiens (man)  
C; Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 31-Dec-2000  
C; References: GB:AF032108; NID:92897115; PIDN:MAC39708.1; PMID:92897116  
A; Jeung, E.; Lim, S.P.; Berg, R.; Yang, Y.; Ni, J.; Wang, S.; Krissansen, G.W.  
Biophys. Res. Commun. 243, 317-325, 1998  
A; Title: A novel extracellular domain variant of the human integrin alpha7 subunit gene  
A; Reference number: JC950; MUID:98139911; PMID:947324

A; Molecule type: mRNA  
A; Status: preliminary  
A; Residues: 1-1137 <LEU1>  
A; Cross-references: GB:AF032108; NID:92897115; PIDN:MAC39708.1; PMID:92897116  
A; Accession: JC951

A; Molecule type: mRNA  
A; Status: preliminary  
A; Residues: 1-657-733-1137 <LEU2>  
A; Cross-references: GB:AF032108  
R; Wang, W.; Wu, W.; Desai, T.; Ward, D.C.; Kaufman, S.J.  
Genomics 26, 563-570, 1995  
A; Title: Localization of the alpha7 integrin gene (ITGA7) on human chromosome 12q13: cDNA  
A; Reference number: A56839  
A; Molecule type: mRNA  
A; Status: preliminary  
A; Residues: 664-668-668-688-690-825-'X'-827-839-'D'-841-946-'H'-948-'T'-951-'P'-953-1052  
A; Cross-references: EMBL:X72495; NID:9437781  
R; Song, W.K.; Wang, W.; Sato, H.; Bieser, D.; Kaufman, S.  
submitted to the EMBL Data Library, July 1993  
A; Description: Expression of alpha 7 integrin cytoplasmic domains during skeletal muscle  
phototaxis.  
A; Reference number: S40147  
A; Accession: S40147  
A; Molecule type: mRNA  
A; Residues: 1061-1137 <SON>  
C; Genetics:

A; Gene: GDB:ITGA7  
A; Cross-references: EMBL:X72495; NID:9437781; PIDN:CAA52348.1; PMID:9437782

Query Match Score 46.5; DB 2; Length 1137;  
Best Local Similarity 47.8%; Pred. No. 94; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
Matches 11; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 2 DLQERGDNF---SPFSGCQPF 21  
Db 390 DLNQDGFPDIAGAPFDGDSKVF 412

---

RESULT 13

AD154 nucleotidyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C; Species: Agrobacterium tumefaciens  
C; Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

C; Accession: AD3154  
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Levy, R.; Li, M.; McClellan, E.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavina, T.; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.; ster, E.W.  
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A; Reference number: AB2577; MUID:21608550; PMID:11743193

A; Accession: AD3154

A; Status: preliminary

A; Molecule type: DNA  
A; Residues: 1-308 <KUR>

A; Cross-references: GB:AE008689; PIDN:AAL45650.1; PMID:917743374; GSPDB:GN00187

A; Experimental source: strain C58 (Dupont)

C; Genetics:

A; Gene: Atu4856

A; Map position: linear chromosome

Query Match Score 46%; DB 2; Length 308;  
Best Local Similarity 60.0%; Pred. No. 26;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 GNDNDISPGSGDGPFF 21  
Db 112 GAREISNFLNDGPFF 126

---

RESULT 14

E98133 hypothetical protein AGR\_L\_62 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C; Species: Agrobacterium\_tumefaciens

C; Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002

C; Accession: E98133

R; Goodner, B.; Hinkle, G.; Gartung, S.; Miller, N.; Qurollo, B.; Goldman, B.; Liu, F.; Hollman, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A; Reference number: A97359; MUID:21608551; PMID:11743194

A; Accession: E98133

A; Status: preliminary

A; Molecule type: DNA  
A; Residues: 1-365 <KUR>

A; Cross-references: GB:AE007870; PIDN:AAK88591.1; PMID:915158304; GSPDB:GN00170

A; Gene: AGR\_L\_62

A; Map position: linear chromosome

Query Match Score 46%; DB 2; Length 365;  
Best Local Similarity 60.0%; Pred. No. 32;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 GNDNDISPGSGDGPFF 21  
Db 169 GAREISNFLNDGPFF 183

---

RESULT 15

A83170 S-adenosylmethionine-tRNA ribosyltransferase-isomerase (EC 5.4.99.-) queA PA3824 [similar]

C; Species: Pseudomonas aeruginosa

C; Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C; Accession: A83170

R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brzadlman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lazbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A; Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho-

A; Reference number: A82950; MUID:20437337; PMID:10984043  
A; Accession: A83170  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-347 <STO-  
A; Cross-references: GB:AE004799; GB:AE004091; NID:9949981; PIDN:AAG07211.1; GSPDB:GN001  
A; Experimental source: strain PAO1  
C; Genetics:  
A; Gene: queA; PA1824  
C; Superfamily: Escherichia coli tRNA ribouridyltransferase-isomerase  
C; Keywords: intramolecular transferase; isomerase  
Query Match Similarity 42.9%; Score 45.5; DB 2; Length 347;  
Best Local Similarity 42.9%; Pred. No. 36;  
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;  
Qy 8 DNIDISPPFSCD-----GQPF 21  
Db 263 DGELKPKFSSDTDIFYGRPF 283

Search completed: January 29, 2004, 12:40:57  
Job time : 17.3421 secs

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Scoring table:	BLOSUM62	
Gapop:	10.0	Gapext 0.5
Searched:	127863 seqs,	47026705 residues
Total number of hits satisfying chosen parameters:	127863	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing First 45 summaries	
Database :	SwissProt_41:	*
	Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
		SUMMARIES
Result No.	Score	Query Match Length DB ID Description
1	52	41.3 301 1 P011_RHOCA
2	49.5	39.3 1259 1 CAML_RAT
3	48	38.1 385 1 LEF3_NPYAC
4	46.5	36.9 1106 1 ITA7_RAT
5	46.5	36.9 1179 1 ITA7_MOUSE
6	46.5	36.9 1181 1 ITA7_HUMAN
7	45.5	36.1 347 1 QEA_PSEAE
8	45.5	36.1 1015 1 ITA4_DROME
9	45.5	36.1 1260 1 CAML_MOUSE
10	45	35.7 301 1 TSA2_MOUSE
11	45	35.7 309 1 TSA2_HUMAN
12	45	35.7 393 1 GUN1_UTMMA
13	45	35.7 472 1 SACH_BACAM
14	45	35.7 508 1 VLI HPV60
15	45	35.7 851 1 YDBG_SCHPO
16	44.5	35.3 698 1 YJBH_ECOLI
17	44.5	35.3 1050 1 ITA5_XENLA
18	44	34.9 348 1 NTCI_CRIGR
19	44	34.9 475 1 DEGP_SALTY
20	43.5	34.5 284 1 RL2_CHLMU
21	43.5	34.5 284 1 RL2_CHLTR
22	43	34.5 631 1 COBT_PSEDE
23	43.5	34.5 1053 1 ITA5_MOUSE
24	43	34.5 1115 1 ITA3_DROME
25	43	34.1 209 1 COEC_SCYCA
26	43	34.1 684 1 RPSD_AGRTS
27	43	34.1 3703 1 ABF1_HUMAN
28	43	34.1 3726 1 ABF1_MOUSE
29	42.5	33.7 488 1 FA10_HUMAN
30	42.5	33.7 1000 1 ITA5_DROME
31	42	33.3 119 1 GVO1_HALN2
32	42	33.3 120 1 GVO1_HALN2
33	42	33.3 224 1 DCL_LYCSES
34	42	33.3 269 1 MHPD_ECOLI
35	42	33.3 269 1 WBP1_HUMAN
36	42	33.3 294 1 Y354_CLOSE
		P092Bk1_rhizobium_m
		37 42 33.3 359 1 HRCA_RHIME
		38 42 33.3 445 1 SLP2_DROME
		39 42 33.3 557 1 FILIP_RHIME
		40 42 33.3 823 1 SYL_DETRA
		41 42 33.3 941 1 AKV1_HUMAN
		42 42 33.3 1192 1 METH_MCTU
		43 42 33.3 1756 1 TR11_ECOLI
		44 41.5 32.9 232 1 VRBD_BT73
		45 41.5 32.9 265 1 FABH_ECOLI



FT	CARBODY	968	968	N-LINKED (GLCNAC, .) (POTENTIAL).		RESULT 4
FT	CARBODY	978	978	N-LINKED (GLCNAC, .) (POTENTIAL).		ITTA7 RAT STANDARD; PRT; 1106 AA.
FT	CARBODY	1021	1021	N-LINKED (GLCNAC, .) (POTENTIAL).	ID ITTA7 RAT ID ITTA7 RAT STANDARD; PRT; 1106 AA.	
FT	CARBODY	1029	1029	N-LINKED (GLCNAC, .) (POTENTIAL).	AC 063026; Q63026; 063027;	
FT	CARBODY	1072	1072	N-LINKED (GLCNAC, .) (POTENTIAL).	DT 16-Oct-2001 (Rel. 40, Created)	
FT	CARBODY	1106	1106	N-LINKED (GLCNAC, .) (POTENTIAL).	DT 16-Oct-2001 (Rel. 40, Last sequence update)	
FT	VARSPLIC	1179	1182	Missing (in isoform 2).	DT 28-Feb-2003 (Rel. 41, Last annotation update)	
FT				/FTID=VSP_002592.	DB Integрин alpha-7 (H36-alpha7).	
SQ	SEQUENCE	1259 AA;	140934 MW;	OFL2ATC415F3C08 CRC64;	GN ITGA7.	
Query Match	Score 39.3%;	Score 49.5%;	DB 1;	Length 1259;	OS Rattus norvegicus (Rat).	
Best Local Similarity	66.7%;	Pred. No. 13;			OC Bukarystoa; Metzoza; Chordata; Craniata; Vertebrata; Euteleostomi;	
Matches 12;	Conservative	1;	Mismatches 4;	Indels 1;	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
Qy	2 DLQERGDNDISPGSGDQ 19				NCBI_TaxID=10116;	
Db	558 DLQERGDSD-KYFIEDGQ 574				RN RP SEQUENCE FROM N.A. (ISOFORM ALPHA-7X1B).	
RESULT 3	LEF3 NPVAC	STANDARD;	PRT;	385 AA.	RX TISSUE=Skeletal muscle;	
AC	P41453;				RC MEDLINE=92242309; PubMedId=1315319;	
DT	01-NOV-1995 (Rel. 32, Created)				RA Song W.K., Wang W., Foster R.F., Bielser D.A., Kaufman S.J.;	
DT	01-NOV-1997 (Rel. 32, Last sequence update)				"H36-alpha 7 is a novel integrin alpha chain that is developmentally	
DT	01-NOV-1997 (Rel. 35, Last annotation update)				regulated during skeletal myogenesis.";	
DB	Late expression factor 3.				RA J. Cell Biol. 117:643-657 (1992).	
GN	LEF-3.				RN [2]	
OS	Autographa californica nuclear polyhedrosis virus (AcMNPV).				RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X1A AND ALPHA-7X1C).	
OC	Viruses; dsDNA viruses, no RNA Stage; Baculoviridae;				RC TISSUE=Skeletal muscle;	
OC	Nucleopolyhedrovirus.				RC MEDLINE=94171924; PubMedId=8126096;	
NCBI_TaxID=46015;					RA RA "Expression of alpha 7 integrin cytoplasmic domains during skeletal	
RN					RT RT muscle development: alternate forms, conformational change, and	
RC					RT RT homologies with serine/threonine kinases and tyrosine phosphatases."	
RC					J. Cell Sci. 106:1139-1152 (1993).	
RC					RN [3]	
RC					RP TISSUE SPECIFICITY.	
RC					RX MEDLINE=96197133; PubMedId=8626012;	
RC					RA Martin P.T., Kaufman S.J., Kramer R.H.J., Sanoes J.R.;	
RC					RT "Synaptic integrins in developing, adult, and mutant muscle: selective	
RC					RT association of alpha1, alpha7, and alpha7B integrins with the	
RC					RT neuromuscular junction";	
RC					RL Dev. Biol. 174:125-139 (1996).	
RC					CC -1- FUNCTION: INTEGRIN ALPHAI-7/BETA-1 IS THE PRIMARY LAMININ RECEPTOR	
RC					CC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC	
RC					CC DIFFERENTIATION, IT MAY INDUCE CHANGES IN THE SHAPE AND MOBILITY	
RC					CC OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH	
RC					CC SITES OF SECONDARY FIBER FORMATION, INVOLVED IN THE MAINTENANCE OF	
RC					CC THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR ANCHORAGE,	
RC					CC VIABILITY AND FUNCTIONAL INTEGRITY.	
RC					CC -1- SUBUNIT: HETERO DIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA	
RC					CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A	
RC					CC DISULFIDE BOND. ALPHAI-7 ASSOCIATES WITH BETA-1.	
RC					CC -1- SUBCELLULAR LOCATION: Type I membrane protein.	
RC					CC -1- ALTERNATIVE PRODUCTS: Event-alternative splicing; Named isoforms=3;	
RC					CC Comment-additional isoforms seem to exist;	
RC					CC Name=Alpha-7X1B;	
RC					CC IsoId=Q61258-1; Sequence=Displayed;	
RC					CC Name=Alpha-7X1A;	
RC					CC IsoId=Q61258-2; Sequence=VSP_002734;	
RC					CC Name=Alpha-7X1C;	
RC					CC IsoId=Q61258-3; Sequence=VSP_002735;	
DR	L18873; AAA02964.1;				CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL AND CARDIAC MUSCLE	
DR	EMBL; L22858; AAA66697.1;				CC EXPRESSED IN REPlicATING MYOBLASTS. IN DIFFERENTIATED MUSCLE	
DR	-				CC FIBERS LOCALIZES BETWEEN FIBERS AND THE SURROUNDING MATRIX.	
DR	D72859; D72858.				CC ISOFORMS A AND B ARE EXPRESSED AT MYOTENDINOUS AND NEUROMUSCULAR	
KW	Early protein; transcription regulation; DNA-binding.				CC FUNCTIONS; ISOFORM C IS EXPRESSED AT NEUROMUSCULAR JUNCTIONS AND	
CC	SEQUENCE 385 AA; 44551 MW;				CC AT EXTRASYNAPTIC SITES.	
CC	OFL2ATC415F3C08 CRC64;				CC -1- DEVELOPMENTAL STAGE: ISOFORMS ARE DEVELOPMENTALLY REGULATED DURING	
CC					CC THE FORMATION OF SKELETAL MUSCLE. ISOFORMS A AND C ARE INDUCED	
CC					CC UPON TERMINAL MYOGENIC DIFFERENTIATION; ISOFORM B IS PRESENT	
CC					CC EARLIER IN REPLICATING CELLS AND DIMINISHES UPON DIFFERENTIATION.	
CC					CC -1- PTM: ADP-RIBOSYLATED ON AT LEAST TWO SITES IN THE EXTRACELLULAR	
CC					CC DOMAIN IN SKELETAL MYOTUBES (BY SIMILARITY).	
CC					CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.	
CC					CC -1- SIMILARITY: Contains 7 FG-GAP repeats.	



RX MEDLINE=95238432; PubMed=7721841;

RA Zolothska A.; Moss J.;  
RA "Processing of ADP-ribosylated integrin alpha 7 in skeletal muscle myotubes.",  
J. Biol. Chem. 270:9227-9233 (1995).

CC - FUNCTION: INTEGRIN ALPHA-7/BETA-1 IS THE PRIMARY LAMININ RECEPTOR ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC DIFFERENTIATION, IT MAY INDUCE CHANGES IN THE SHAPE AND MOBILITY OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH SITES OF SECONDARY FIBER FORMATION. INVOLVED IN THE MAINTENANCE OF THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR ANCHORAGE, VIABILITY AND FUNCTIONAL INTEGRITY. MICE CARRYING A ITGα7 NULL ALLELE ARE Viable AND FERTILE, BUT SHOW PROGRESSIVE MUSCULAR DYSTROPHY STARTING SOON AFTER BIRTH, BUT WITH A DISTINCT VARIABILITY IN DIFFERENT MUSCLE TYPES.

CC - SUBUNIT: HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULFIDE BOND. ALPHA-7 ASSOCIATES WITH BETA-1.

CC - SUBCELLULAR LOCATION: Type I membrane protein.

CC - ALTERNATIVE PRODUCTS:

CC - ALTERNATIVE splicing: Named isoforms=6; Comment: Additional isoforms seem to exist. There is a combination of at least four alternatively spliced domains, extracellular (X1 and X2), and two cytoplasmic (A and B). A third potential alternatively spliced cytoplasmic domain (C) doesn't appear to be expressed. So far detected are isoforms alpha-7X alpha-7X B and alpha-7X B. Experimental confirmation may be lacking for some isoforms;

Name=Alpha-7X1X2B;  
IsoID=Q61738-1; Sequence=Displayed;

CC Name=Alpha-7X1A;  
IsoID=Q61738-2; Sequence=VSP\_002732; VSP\_002733;

CC Name=Alpha-7X1B;  
IsoID=Q61738-3; Sequence=VSP\_002732;

CC Name=Alpha-7X2A;  
IsoID=Q61738-4; Sequence=VSP\_002731; VSP\_002733;

CC Name=Alpha-7X2B;  
IsoID=Q61738-5; Sequence=VSP\_002731;

CC - TISSUE SPECIFICITY: ISOFORMS CONTAINING SEGMENT X2 ARE FOUND IN ADULT HEART, LUNG AND SKELETAL MUSCLE. ISOFORMS CONTAINING SEGMENT X1 ARE EXPRESSED IN ADULT HEART, LONG AND IN PROLIFERATING SKELETAL MYOBLASTS BUT NOT IN ADULT SKELETAL MUSCLE. ISOFORMS CONTAINING SEGMENT A ARE EXCLUSIVELY FOUND IN SKELETAL MUSCLE. ISOFORMS CONTAINING SEGMENT B ARE WIDELY EXPRESSED IN MUSCLE FIBERS. ISOFORMS CONTAINING SEGMENT A AND B ARE EXPRESSED AT MYOTENDINOUS AND NEUROMUSCULAR JUNCTIONS, ISOFORMS CONTAINING SEGMENT C ARE EXPRESSED AT NEUROMUSCULAR JUNCTIONS AND AT EXTRASYNAPTIC SITES.

CC - DEVELOPMENTAL STAGE: ISOFORMS ARE DEVELOPMENTALLY REGULATED DURING FORMATION OF SKELETAL MUSCLE. UNDIFFERENTIATED (REPLICATING) MYOBLASTS EXPRESS ISOFORMS CONTAINING SEGMENT B ONLY, WHEREAS DIFFERENTIATED MYOBLASTS EXPRESS ISOFORMS CONTAINING SEGMENTS A B.

CC - PTM: ADP-RIBOSYLATED ON AT LEAST TWO SITES OF THE EXTRACELLULAR DOMAIN IN SKELETAL MYOTUBES (IN VITRO).

CC - SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

CC - SIMILARITY: Contains 7 FG-GAP repeats.

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CC EMBL: L23423; AAA16600.1; -;  
DR EMBL: U60419; AAC52772.1; -;  
DR EMBL: Y12380; CAAT3023.1; -;  
DR EMBL: W12383; CAAT3023.1; JOINED;  
DR EMBL: Y12384; CAAT3023.1; JOINED;

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Integrin alpha-7 precursor.  
 GN ITGA7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI TaxID=9606;  
 RN [1] \_  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-7X2B AND ALPHA-7X2DB).  
 RC TISSUE=Petal heart, and Osteoblast;  
 RX MEDLINE=98139911; PubMed=9413524;  
 RA Leung E., Lim S.P., Berg R., Yang Y., Ni J., Wang S.-X.,  
 RA Krissansen G.W.;  
 RT "A novel extracellular domain variant of the human integrin alpha 7  
 subunit generated by alternative intron splicing.";  
 RL Biochem. Biophys. Res. Commun. 243:317-325(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2B).  
 RX MEDLINE=98250181; PubMed=9530299;  
 RA Hayashi Y.K., Chou F.-L., Engvall E., Ogawa M., Matsuda C.,  
 RA Hirabayashi S., Yokochi K., Ziobor B.L., Kramer R.H., Kaufman S.J.,  
 RA Ozawa E., Goto Y.-I., Nonaka I., Tsukahara T., Wang J.Z.,  
 RA Hoffman B. P., Arakata K.;  
 RT "Mutations in the integrin alpha 7 gene cause congenital myopathy."  
 RL Nat. Genet. 19:94-97(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2B).  
 RA Vizirianakis I.S., Ziobor B.L., Kramer R.H.,  
 RT "Cloning of human integrin alpha-7 cDNA";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.  
 TISSUE=Skeletal muscle;  
 RX MEDLINE=99333684; PubMed=10403775;  
 RA Vignier N., Moghadaszadeh B., Gary F., Beckmann J., Mayer U.,  
 RA Guicheny P.;  
 RT "Structure, genetic localization, and identification of the cardiac  
 and skeletal muscle transcripts of the human integrin alpha 7 gene  
 (ITGA7)." ;  
 RL Biochem. Biophys. Res. Commun. 260:357-364(1999).  
 RN [5]  
 RP SEQUENCE OF 34-45.  
 RC TISSUE=Melanoma;  
 RX MEDLINE=92199882; PubMed=1819357;  
 RA Ziobor B.L., Vu M.P., Cheng Y.F., Ramos D.M., Timpl R., Waleh N.;  
 RT Kramer R.H., Vu M.P., Cheng Y.F.;  
 RT "Laminin-binding integrin alpha 7 beta 1: functional characterization  
 and expression in normal and malignant melanocytes.";  
 RL Cell Regul. 2:805-817(1991).  
 RN [6]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-7X2).  
 TISSUE=Heart;  
 RX MEDLINE=94075378; PubMed=82353814;  
 RA Ziobor B.L., Vu M.P., Waleh N., Crawford J., Lin C.-S., Kramer R.H.;  
 RT "Alternative extracellular and cytoplasmic domains of the integrin  
 alpha 7 subunit are differentially expressed during development.";  
 RL J. Biol. Chem. 268:26773-26783(1993).  
 RN [7]  
 RP SEQUENCE OF 1105-11181 FROM N.A. (ISOFORM ALPHA-7B).  
 TISSUE=Petal muscle;  
 RX MEDLINE=9417924; PubMed=8126096;  
 RA Song W.K., Wang W., Sato H., Bielemer D.A., Kaufman S.J.;  
 RT "Expression of alpha 7 integrin cytoplasmic domains during skeletal  
 muscle development: alternate forms, conformational change, and  
 homologies with serine/threonine kinases and tyrosine phosphatases.";  
 RL J. Cell Sci. 106:1139-1152(1993).  
 RN [8]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-7A).  
 TISSUE=Skeletal muscle;  
 RX MEDLINE=98012902; PubMed=9352853;  
 RA Basora N., Vachon P.R., Herring-Gilliam F.E., Petreault N.,  
 RA Beaulieu J.-F.;  
 RN [9]  
 RP FUNCTION;  
 RX MEDLINE=97453229; PubMed=9307969;  
 RA Ziobor B.L., Chen Y.Q., Kramer R.H.;  
 RT "The laminin-binding activity of the alpha 7 integrin receptor is  
 defined by developmentally regulated splicing in the extracellular  
 domain";  
 RT Mol. Biol. Cell 8:1723-1734 (1997).  
 RN [10]  
 RP FUNCTION;  
 RX MEDLINE=20160722; PubMed=10694445;  
 RA Schoeberl S., Mielenz D., Borchtermayer F., Hapke S., Poeschl E.,  
 RA von der Mark H., Moch H., von der Mark K.;  
 RT "The role of extracellular and cytoplasmic splice domains of  
 alpha 7-integrin in cell adhesion and migration on laminins.";  
 RL Exp. Cell Res. 255:303-313(2000).  
 RN [11]  
 RP TISSUE SPECIFICITY;  
 RX MEDLINE=96197133; PubMed=8526012;  
 RA Martin P.T., Kaufman S.J., Kramer R.H., Sanes J.R.;  
 RT "Synaptic integrins in development, adult, and mutant muscle: selective  
 association of alpha 1, alpha 7A, and alpha 7B integrins with the  
 neuromuscular junction.";  
 RL Dev. Biol. 174:125-139(1996).  
 CC -!- FUNCTION: INTEGRIN ALPHA-7/BETA-1 IS THE PRIMARY LAMININ RECEPTOR  
 CC ON SKELETAL MYOBLASTS AND ADULT MYOFIBERS. DURING MYOGENIC DIFFERENTIATION, IT MAY INDUCE CHANGES IN THE SHAPE AND MOBILITY  
 CC OF MYOBLASTS, AND FACILITATE THEIR LOCALIZATION AT LAMININ-RICH  
 CC SITES OF SECONDARY FIBER FORMATION. IT IS INVOLVED IN THE MAINTENANCE OF THE MYOFIBERS CYTOARCHITECTURE AS WELL AS FOR THEIR  
 CC ANCHORAGE, VIABILITY AND FUNCTIONAL INTEGRITY. ISOFORMS ALPHA-7X2B AND ALPHA-7X1B PROMOTE MYOBLAST MIGRATION ON LAMININ 1 AND LAMININ  
 CC 2/4, BUT ALPHA-7X1B IS LESS ACTIVE ON LAMININ 1 (IN VITRO).  
 CC -!- SUBUNIT: HETEROODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA  
 CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULFIDE BOND. ALPHA-7 ASSOCIATES WITH BETA-1.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=12;  
 CC Comment=Additional isoforms seem to exist. There is a combination of at least five alternatively spliced domains, three extracellular (X1, X2 and D) and two cytoplasmic (A and B). A third potential alternatively spliced cytoplasmic domain (C) does not appear to be expressed. In vitro generated isoform X2C shows function. So far detected are isoforms Alpha-7X1A, Alpha-7X2B (major), Alpha-7X2D (minor) and minor isoforms containing segment 'X1X2'. Experimental confirmation may be lacking for some isoforms;  
 CC Name=Alpha-7X1X2B;  
 CC TsoId=Q13683-1; Sequence=Displayed;  
 CC Name=Alpha-7X1A;  
 CC IsoId=Q13683-2; Sequence=VSP\_002728; VSP\_002730;  
 CC Name=Alpha-7X1B;  
 CC IsoId=Q13683-3; Sequence=VSP\_002728;  
 CC Name=Alpha-7X1DA;  
 CC IsoId=Q13683-4; Sequence=VSP\_002728; VSP\_002730;  
 CC Name=Alpha-7X1DB;  
 CC IsoId=Q13683-5; Sequence=VSP\_002728; VSP\_002729;  
 CC Name=Alpha-7X2A;  
 CC IsoId=Q13683-6; Sequence=VSP\_002727; VSP\_002730;  
 CC Name=Alpha-7X2B;  
 CC IsoId=Q13683-7; Sequence=VSP\_002727;  
 CC Name=Alpha-7X2DA;  
 CC IsoId=Q13683-8; Sequence=VSP\_002727; VSP\_002730;  
 CC Name=Alpha-7X2DB;  
 CC IsoId=Q13683-9; Sequence=VSP\_002727; VSP\_002730;  
 CC Name=Alpha-7X1X2A;  
 CC IsoId=Q13683-10; Sequence=VSP\_002730;  
 CC Name=Alpha-7X1X2DA;  
 CC IsoId=Q13683-11; Sequence=VSP\_002729; VSP\_002730;



RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D., Wan R.H., Doyle C., Baxter G., Heit G., Nelson C.R., Miklos G.L.G., Abril J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballieu R.M., Basu A., Boxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernari D., Bolshakov S., Borckow D., Botchan M.R., Bouck J., Brothman P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Cherry J.M., Cowley S., Dahlke B., Davies P., Davenport B., Delcher A., Deng Z., Days A.D., Dew I., Dietz S.M., Dodge K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fostier C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris D., Harvey D., Hernandez J.R., Houck J., Houston K.A., Houston T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milash N.V., Moberly C., Morris J., Mosheri A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., PurI V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spreading A.C., Stimpleton M., Strong R., Sun E., Sun R., Svärkskars R., Tector C., Turner E., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L., Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.Q., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> "; RT RL Science 287:2185-2195 (2000).	PT	CARBOHYD	455	455	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	589	589	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	746	746	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	821	821	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	842	842	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	853	853	N-LINKED (GLCNAC. . .)	(POTENTIAL).	PT	CARBOHYD	877	877	N-LINKED (GLCNAC. . .)	(POTENTIAL).	SO	SEQUENCE	1015	AA:	112761 MW:	964BEB424FB1FBC6 CRC64;
RA	Query Match 36.1%; Best Local Similarity 39.1%; Matches 9; Conservatve 6; Mismatches 5; Indels 3; Gaps 1;	Qy	2 DLOERGNDI---SPFSGDGPFF 21	Db	343 DINKDGYNDVAVGAPFAGNGSVF 365																																																		
RA	RESULT 9 CAML MOUSE ID_CAML MOUSE STANDARD; PRT: 1260 AA.	RA	AC P1.627;	RA	DT 01-OCT-1989 (Rel. 12, Created)																																																		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., PurI V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sieden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spreading A.C., Stimpleton M., Strong R., Sun E., Sun R., Svärkskars R., Tector C., Turner E., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L., Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.Q., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> "; RT RL Science 287:2185-2195 (2000).	RA	DT 01-OCT-1989 (Rel. 12, Last sequence update)																																																				
RA	RA	DT 01-SEP-2003 (Rel. 42, Last annotation update)																																																					
RA	RA	DE Neural cell adhesion molecule LI precursor (N-CAM LI).																																																					
RA	RA	GN LI CAM OR CAMLI.																																																					
RA	RA	OS Mus musculus (Mouse).																																																					
RA	RA	OC Buxarioria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.																																																					
RA	RA	OC NCBI_TaxID=10090;																																																					
RA	RA	RN [1]																																																					
RA	RA	RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.																																																					
RA	RA	RC TISSUE=brain; MEDLINE=88318924; PubMed=3412448;																																																					
RA	RA	RT Moos M., Tacke R., Scherer H., Teplow D., Frueh K., Schachner M.; "Neural adhesion molecule LI as a member of the immunoglobulin superfamily with binding domains similar to fibronectin."																																																					
RA	RA	RL Nature 334:701-703 (1988).																																																					
RA	RA	CC - FUNCTION: CELL ADHESION MOLECULE WITH AN IMPORTANT ROLE IN THE DEVELOPMENT OF THE NERVOUS SYSTEM, INVOLVED IN NEURON-NEURON. BINDS ADHESION NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS TO AXONIN ON NEURONS.																																																					
RA	RA	CC - SUBCELLULAR LOCATION: TYPE I membrane protein.																																																					
RA	RA	CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.																																																					
RA	RA	CC - SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.																																																					
RA	RA	CC - SIMILARITY: Contains 5 fibronectin type III domains.																																																					
RA	RA	CC - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to licenses@isb-sib.ch).																																																					
RA	RA	CC - EMBL: X12875; CA831368.1; - . .																																																					
RA	RA	CC - DR EMBL: X12875; CA831368.1; - . .																																																					
RA	RA	CC - DR PIR; S05479; S05479.																																																					
RA	RA	CC - DR HSSP; P20241; ICPB.																																																					
RA	RA	CC - DR MGD; MGI:96721; Licam.																																																					
RA	RA	CC - DR InterPro; IPR03361; PN_III.																																																					
RA	RA	CC - DR InterPro; IPR03006; Ig_C2.																																																					
RA	RA	CC - DR InterPro; IPR07110; Ig_MHC.																																																					
RA	RA	CC - DR Pfam; PF00047; Ig_6.																																																					
RA	RA	CC - DR SMART; SM00666; FN3; 2.																																																					
RA	RA	CC - DR PROSITE; PS00835; Ig_LIKE.																																																					
RA	RA	CC - DR KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain; Immunoglobulin domain; Signal.																																																					
RA	RA	CC - SIGNAL 1 19																																																					

FT	CHAIN DOMAIN	20	1260	NEURAL CELL ADHESION MOLECULE L1.
FT	TRANSMEM	1123	1123	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	1124	1146	POTENTIAL.
FT	DOMAIN	1147	1260	IG-LIKE C2-TYPE 1.
FT	DOMAIN	135	130	IG-LIKE C2-TYPE 2.
FT	DOMAIN	138	225	IG-LIKE C2-TYPE 3.
FT	DOMAIN	239	419	IG-LIKE C2-TYPE 4.
FT	DOMAIN	332	506	IG-LIKE C2-TYPE 5.
FT	DOMAIN	424	506	IG-LIKE C2-TYPE 6.
FT	DOMAIN	517	896	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	827	994	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	932	1094	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	1032	553	CELL ATTACHMENT SITE (POTENTIAL).
FT	SITE	562	564	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	57	113	BY SIMILARITY.
FT	DISULFID	157	208	BY SIMILARITY.
FT	DISULFID	263	311	BY SIMILARITY.
FT	DISULFID	353	403	BY SIMILARITY.
FT	DISULFID	447	496	BY SIMILARITY.
FT	DISULFID	538	590	BY SIMILARITY.
FT	CARBOHYD	100	100	(POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	504	504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	587	587	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	725	725	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	776	776	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	824	824	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	848	848	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	875	875	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	968	968	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	978	978	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1022	1022	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1030	1030	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1073	1073	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1107	1107	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1260	AA;	140968 MW;
				22BB57001ICB2A538 CRC64;
				Query Match Score 36.1%; Best Local Similarity 61.1%; Pred. No. 55; Length 1260; Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
Qy	2	DQ0ERGDNDISPGSGDQQ	19	
Db	558	DQ0ERGDSD-KYTEDGK	574	
RESULT 10				
ID	"TSA2 MOUSE STANDARD; Q8VIG3; Q9DALS;"			PRT; 301 AA.
AC				Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Testis-specific gene A2 (Male meiotic metaphase acidic protein) (Meichroacidin).			
GN	TSGA2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISSUE-TESTIS;			
RX	MEDLINE-98246622; PubMed=9578619;			
RA	Truchica J., Nishina Y., Wakabayashi N., Nozaki M., Sakai Y., Nishimune Y.,			

"Molecular cloning and characterization of meichroacidin (male meiotic metaphase chromosome-associated acidic protein)." Dev. Biol. 197:67-76 (1998).

RT RT metaphase chromosome-associated acidic protein".

RL RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Saito R., Saito T., Okajobi Y., Gojobori T., Bono H., Kasukawa T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gibbs C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincovich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez J., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seye T., Shiba Y., Storch K.-P., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; RT "Functional annotation of a full-length mouse cDNA collection." Nature 409:685-690 (2001).

CC -1- FUNCTION: The specific expression during male germ cell development and its characteristic localization suggest that it may play an important role in male meiosis.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic in late spermatocytes, secondary spermatocytes and round spermatids. Gathered around metaphase chromosomes during meiotic divisions.

CC -1- ALTERNATIVE PRODUCTS:

CC -1- Event=Alternative splicing; Named isoforms=2;

CC -1- Note=No experimental confirmation available;

CC -1- Name=1;

CC -1- IsoID=Q8VIG3-1; Sequence=Displayed;

CC -1- Name=2;

CC -1- IsoID=Q8VIG3-2; Sequence=Not described;

CC -1- Name=3;

CC -1- Note=No experimental confirmation available;

CC -1- TISSUE-SPECIFICITY: Germ cell specific. Specifically expressed in testis, and to a lower extent in ovary. Not expressed in somatic tissues.

CC -1- DEVELOPMENTAL STAGE: During male germ cell development it is not detected until 12 days. Significant expression is detected from 14-day-old through to adult testis. Expression is first detected in the pachytene spermatocytes at stage V, becomes stronger from the late pachytene spermatocytes to round spermatid stage, and then gradually decreases as the morphogenesis proceeds further. Not expressed in germ cells located in the first layer of the seminiferous epithelium (spermatogonia, leptotene and zygote spermatocytes).

CC -1- SIMILARITY: Contains 6 MORN repeats, CC -1- SIMILARITY: Ref.1 sequence differs from that shown due to a frameshift in position 283.

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CC -----

CC DR AB005535; BAB83693\_1; ALT\_FRAME.

CC DR EMBL; AK005739; BAB24214\_1; -.

CC DR MGD; MGI:1194909; Tspz2.

CC DR InterPro; IPR01409; MORN.

CC DR PF02493; MORN; 6.

CC DR SMART; SM00698; MORN; 6.

CC DR Meiosis; Repeat; Alternative splicing.

CC FT DOMAIN; 195 201 POLY-GUU.

CC RA REPEAT 20 43 MORN 1.

Query Match 35.7%; Score 45; DB 1; Length 301;  
 Best Local Similarity 37.5%; Pred. No. 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DLQERGNDNDISPFSGD 17  
 Db 8 ELEEEEGENDIGEYEG 23

RESULT 12

QUNI\_USTMIA STANDARD; PRT; 393 AA.

ID QUNI\_USTMIA  
 AC P34424;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1)  
 EG1  
 GN Utilago maydis (Smut fungus).  
 OS Utilago maydis (Smut fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginales; Ustilaginaceae; Ustilago.  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FBD11;  
 RX MEDLINE:96115728; PubMed=8590631;  
 RA Schauwecker F.; Wanner G.; Kahlmann R.;  
 RT "Filament-specific expression of a cellulase gene in the dimorphic  
 fungus *Ustilago maydis".*  
 RL Biol. Chem. Hoppe-Seyler 376:617-625(1995).

-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 linkages in cellulose, lichenin and cereal beta-D-glucans.

CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: HYPHAL TIP.  
 CC -|- DEVELOPMENTAL STAGE: EXPRESSED IN FILAMENTOUS DIKARYON.  
 CC -|- PTM: MAY ALSO BE O-GLYCOSYLATED.  
 CC -|- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL  
 HYDROLASES).

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 or send an email to license@isb-sib.ch).

CC or send an email to license@isb-sib.ch).

CC DR EMBL; S81598; AA336147.1; -.

CC DR PTR; S59499; S59499.

CC DR HSSP; P43316; ZENG.

CC DR InterPro; IPR00334; Glyco hydro\_45.

CC DR Pfam; PF02015; Glyco hydro\_45; 1-

CC DR PROSP; PS01140; GLYCOSYL\_HYDROL\_F45; 1;

CC KW Cellulose degradation; Hydrolase; Glycosidase; Signal; Glycoprotein.

CC FT SIGNAL 1 26

CC FT CHAIN 27 393

CC FT ACT\_SITE 34 34

CC DR ENDOGLUCANASE 1 NUCLEOPHILE (BY SIMILARITY).

CC DR PROTON DONOR (BY SIMILARITY).

CC FT ACT\_SITE 152 152  
 CC DOMAIN 270 385  
 CC CARBOHYD 343 343  
 CC SEQUENCE 393 AA; 39594 MW; 65C753C610CD6A3 CRC64; POTENTIAL.

Query Match 35.7%; Score 45; DB 1; Length 393;  
 Best Local Similarity 61.5%; Pred. No. 17; Mismatches 2; Conservative 3; Indels 0; Gaps 0;

Qy 4 QERGDDNDISPFSG 16

		:      :	
Db	235	QRKDNTTSPYSG	247
RESULT 13			
SACB_BACAM	BACAM	STANDARD;	PRT; 472 AA.
ID	SACB_BACAM		
AC	P21170;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	15-DEC-1998 (Rel. 37, Last annotation update)		
DB	Levanase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase)		
DE			
GN	SACB		
OS	Bacillus amyloliquefaciens.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX			
NCBI_TAXID=1390;			
RN			
[1]			
SEQUENCE FROM N.A.			
RT	"Isolation and characterization of levanase-encoding gene from Bacillus amyloliquefaciens."		
RT	Tang L.B., Lenstra R.R., Borchart T.V., Vasantha N.;		
RT	Gene 96: 89-93 (1990).		
CC	-I- CATALYTIC ACTIVITY: Sucrose + {(2,6)-beta-D-fructosyl} (N) = Glucose + {(2,6)-beta-D-fructosyl} (N+1).		
CC	-I- SUBCELLULAR LOCATION: Secreted.		
CC	-I- INDUCTION: By sucrose.		
CC	-I- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.		
CC			
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CC			
DR	X52988; CAA3179.1; -.		
DR	PIR; JQ0802; JQ0802;		
DR	InterPro; IPR003416; Glyco_hydro_68.		
PFAM	PF024245; Glyco_hydro_68; 1-		
TRANSM	GlycosylTransferase; Signal.		
SIGNAL	1 29		
FT	CHAIN 30 472 AA; LEVANSURFACE.		
SEQ	SEQUENCE 472 AA; 52859 MW; P38592D272677ED CRC64;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RL	[2]		
RN	SEQUENCE OF 372-467 FROM N.A.		
RP			
RA	Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.		
RA	Chan S.Y., Delius H., Hafern A.L., Bernard H.U.;		
RA	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.		
CC			
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CC			
DR	EMBL; U31792; AAA79491.1; -.		
DR	EMBL; U21876; AAA92837.1; -.		
DR	InterPro; IPR002210; PV capsid L1.		
PFAM	PF0530; late_protein_L1;		
PRINTS	PRO0865; HPVAPSPSL1;		
DR	ProdDom; PD000544; PV capsid_L1.		
KW	Coat protein; Late protein.		
SEQUENCE	508 AA; 57827 MW; 314954989534DD0 CRC64;		
Query Match	35.7%; Score 45; DB 1; Length 508;		
Best Local Similarity	64.3%; Pred. No. 23;		
Matches	9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Ox	2 DIQERGNDISPS 15		
Db	459 DIQERFSNELSOFS 472		
RESULT 15			
YDBG_SCHPO	STANDARD;		
ID	YDBG_SCHPO		
AC	YDBG_SCHPO		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Hypothetical protein C22E12.16C in chromosome 1.		
GN	SPAC22E12.16C		
OS	Schizosaccharomyces pombe (Fission yeast).		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomyces; Schizosaccharomyces.		
OC	Schizosaccharomyces; Schizosaccharomycesae.		
OC			
OX	[1] TAXID=4896;		
RN			
RP	SEQUENCE FROM N.A.		
RC	STRAIN=972;		
RX	MEDLINE=21848401; PubMed=11859360;		
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sacuroso J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgeson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Stevens S., Taylor K., Taylor R.G., Trivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrich H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillard C., Talleda V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forssburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,		

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe";  
 RL Nature 415:871-880 (2002).  
 CC -; SIMILARITY: SPRONG, TO YEAST PIK1;  
 CC -; SIMILARITY: BELONGS TO THE PI3/PI-KINASES FAMILY.  
 CC  
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 CC  
 EMBL; Z70043; CAA3903\_1; -  
 DR PIR; T38173; T38173;  
 DR Genedb; SP0022E12\_16c; -  
 DR Spombie; SP0022E12\_16c; -  
 DR InterPro; IPR00043; PI3\_PI4\_kinase.  
 PFam; PF00454; PI3\_PI4\_kinase; 1.  
 SMART; SM00146; PI3KC; 1.  
 PROSITE; PS00915; PI3\_A\_KINASE\_1; 1.  
 DR PROSITE; PS00916; PI3\_A\_KINASE\_2; 1.  
 PROSITE; PS50290; PI3\_A\_KINASE\_3; 1.  
 KW Hypothetical protein; Transferase; Kinase.  
 FT DOMAIN 581 827 PI3K\_PI4K,  
 SEQUENCE 851 AA; 96657 MW; A991F3C7E3D980BE CRC64;  
 Query Match 35.7%; Score 45; DB 1; Length 851;  
 Best Local Similarity 50.0%; Pred. No. 41;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 TDLOERGDDNDISPPSGDG 18  
 Db 382 TNLQDSTDNDISESESEG 399

Search completed: January 29, 2004, 12:39:09  
 Job time : 14.7105 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 29, 2004, 12:35:53 ; Search time 33.8947 Seconds

Title: US-09-812-485A-49  
 Perfect score: 126  
 Sequence: TDLORGNDNDISPFSGDQPFKD 23Scoring table: BLOSUM62  
 Gapext 10.0 , Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
 Maximum Match 10%

Listing First 45 summaries

Database : SPTRMBL23:  
 1: sp\_archea: \*  
 2: sp\_bacteria: \*  
 3: sp\_fungi: \*  
 4: sp\_hexameric: \*  
 5: sp\_invertebrate: \*  
 6: sp\_mammal: \*  
 7: sp\_mhc: \*  
 8: sp\_organelle: \*  
 9: sp\_phage: \*  
 10: sp\_plant: \*  
 11: sp\_rabbit: \*  
 12: sp\_virus: \*  
 13: sp\_vertebrate: \*  
 14: sp\_unclassified: \*  
 15: sp\_virus: \*  
 16: sp\_bacteriap: \*  
 17: sp\_archeap: \*

## ALIGNMENTS

## RESULT 1

Q9NQ76 ID Q9NQ76 PRELIMINARY;

AC Q9NQ76; PRT; 525 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Matrix extracellular phosphoglycoprotein precursor.

GN MEPE, a new gene expressed in bone marrow and tumors causing osteomalacia."

OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TAXID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE:Bone

MEDLINE=2039567; PubMed=10945470;

RA Rose P.S.N., De Zoysa P.A., Dong R., Wang H.R., White K.E.,

RA Econe M.J., Oudet C.L.,

RT "MEPE, a new gene expressed in bone marrow and tumors causing

osteomalacia." Genomics 74:342-351 (2001).

RL Genbank: AJ2276396; CAB97250..1;

DR EMBL: AF323916; AAK70343..1;

DR Genew; HGNC:13361; MEPE.

RT SIGNAL.

PT CHAIN.

FT SIGNAL.

RN 1

RP 17

SEQUENCE 525 AA; 58419 MW;

RX 0977CA6E871CA9E5 CRC64;

Query Match Score 1.26; DB 4; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	126	100.0	525	4	Q9NQ76		Q9NQ76 homo sapien
2	123	97.6	500	6	Q95K65		Q95K65 macaca fasc
3	123	97.6	555	6	Q9NQ76		Q9NQ76 macaca fasc
4	123	97.6	555	6	Q9GM13		Q9GM13 macaca fasc
5	81	64.3	433	11	Q92411		Q92411 mus musculu
6	81	64.3	435	11	Q9BS02		Q9BS02 ratmus norv
7	81	64.3	441	11	Q8KL6		Q8KL6 mus musculu
8	81	64.3	443	11	Q8KS09		Q8KS09 ratmus norv
9	80	63.5	275	4	Q8NC19		Q8NC19 homo sapien
10	53	42.1	423	4	Q8TOP7		Q8TOP7 homo sapien
11	52	41.3	320	2	Q52676		Q52676 rhodobacter
12	50	39.7	356	2	QBL0M4		QBL0M4 uncultured
13	50.	39.7	1007	16	Q8ERB9		Q8ERB9 shewanella
14	49.5	39.3	793	5	Q9VY0		Q9VY0 drosophila
15	49	38.9	326	16	Q8NQY1		Q8NQY1 corynebacte
16	49	38.9	339	2	Q8L0L6		Q8L0L6 uncultured

RESULT 4									
Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TDLQERGNDNDISPFSGDGQPFDK	23						
Db	242	TDLQERGNDNDISPFSGDGQPFDK	264						
<b>RESULT 2</b>									
Q95KG5		PRELIMINARY;		PRT;	500	AA.			
AC	ID	Q95KG5;							
AC	ID	Q95KG5;							
AC	ID	Q95KG5;							
DT	01-DEC-2001	(TREMBLrel.	19,	Created)					
DT	01-DEC-2001	(TREMBLrel.	19,	Last sequence update)					
DT	01-DEC-2001	(TREMBLrel.	19,	Last annotation update)					
DE	Hypothetical protein.								
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;								
NCBI_TaxID=9541;									
SEQUENCE FROM N.A.									
RC	TISSUE=Brain;								
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,								
RA	Suzuki Y., Sugano S., Hashimoto K.;								
RA	"Isolation of full-length cDNA clones from macaque brain cDNA libraries."								
RA	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.								
RL	EMBL; AB050559; BAB17010.1; -.								
DR	AB00891; BAB16894.1; -.								
DR	HYPOTHETICAL protein.								
DR	SEQUENCE 500 AA;	55577 MW;	918D265AD9EDC7BC CRC64;						
<b>RESULT 5</b>									
Qy		PRT;	555	AA.					
Db		Q924I1		PRELIMINARY;					
AC	ID	Q924I1;							
AC	ID	Q924I1;							
AC	ID	Q924I1;							
DT	01-DEC-2001	(TREMBLrel.	19,	Created)					
DT	01-DEC-2001	(TREMBLrel.	19,	Last sequence update)					
DT	01-JUN-2002	(TREMBLrel.	21,	Last annotation update)					
DE	Matrix extracellular phosphoglycoprotein precursor.								
GN	NEPE.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
NCBI_TaxID=1090;									
SEQUENCE FROM N.A.									
RC	STRAIN=C57BL/6J;								
RX	Medline:2130906B; PubMed:11414762;								
RA	Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;								
RA	"Nepe, the gene encoding a tumor-secreted protein in oncogenic hypophosphatemic osteomalacia, is expressed in bone."								
RT	Genomics 74:342-351(2001)								
RT	DR ENSEMBL; AF314364; AAK70342.1; -.								
DR	McG; MGJ:2137384; Mepe.								
KW	SIGNAL.	1	18	POTENTIAL.					
FT	CHAIN 19	433	AA;	45984 MW;	7CD603CAA8CB41B0 CRC64;				
FT	SEQUENCE	433	AA;	45984 MW;	7CD603CAA8CB41B0 CRC64;				
<b>RESULT 3</b>									
Q9N076		PRELIMINARY;		PRT;	555	AA.			
AC	ID	Q9N076;							
AC	ID	Q9N076;							
AC	ID	Q9N076;							
DT	01-OCT-2000	(TREMBLrel.	15,	Created)					
DT	01-OCT-2000	(TREMBLrel.	15,	Last sequence update)					
DT	01-OCT-2000	(TREMBLrel.	15,	Last annotation update)					
DE	Matrix extracellular phosphoglycoprotein.								
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;								
NCBI_TaxID=9541;									
SEQUENCE FROM N.A.									
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,								
RA	Suzuki Y., Sugano S., Hashimoto K.;								
RA	"Isolation of full-length cDNA clones from macaque brain cDNA libraries."								
RA	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AB016056; BAB1638.1; -.								
DR	HYPOTHETICAL protein.								
DR	SEQUENCE 555 AA;	61979 MW;	CCFE1A98ADA19EE4 CRC64;						
<b>RESULT 5</b>									
Qy		PRT;	97.6%	Score 123;	DB 6;	Length 500;			
Db		Q924I1	Best Local Similarity 95.7%;	Pred. No. 2.1e-10;					
Db		Q924I1	Matches 22;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;		
<b>RESULT 6</b>									
Q9ES02		PRT;	95.7%	Score 123;	DB 6;	Length 555;			
Db		Q9ES02	Best Local Similarity 95.7%;	Pred. No. 2.4e-10;					
Db		Q9ES02	Matches 22;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;		

Q9B5O2;	AC	SEQUENCE FROM N.A.	PRT;	443 AA.
DT	ID	Q8K3V0	PRELIMINARY;	
01-MAR-2001	AC	Q8K3V0;		
(TREMBLrel. 16; Last sequence update)	DT	01-OCT-2002	(TREMBLrel. 22; Created)	
01-OCT-2002	DT	01-OCT-2002	(TREMBLrel. 22; Last sequence update)	
Osteoregulin.	OS	01-MAR-2003	(TREMBLrel. 23; Last annotation update)	
Rattus norvegicus (Rat).	OS	DE	Osteoregulin-like protein.	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	OS	Rattus norvegicus (Rat).	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
NCBI_TaxID=10116;	OX	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
[1]	RN	OX	NCBI_TaxID=10116;	
SEQUENCE FROM N.A.	RP	RN	[1]	
STRAIN=Sorague-Dawley;	RC	RP	SEQUENCE FROM N.A.	
MEDLINE=2054963; PubMed=10967096;	RX	RC	STRAIN=F344;	
Petersen D.N., Tkalcic G.T., Mansolf A.L., Rivera-Gonzalez R.,	RA	RA	Wang X., Hu B., Wang Y.,	
Brown T.A.	RA	RA	Rattus norvegicus cDNA sequence expressed in B4 cell line (possible	
"Identification of Osteoblast/Osteocyte Factor 45 (OF45), a Bone-	RT	RT	subtype of osteoregulin".	
specific cDNA Encoding an RGD-containing Protein That Is Highly	RT	RT	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.	
Expressed in Osteoblasts and Osteocytes.,";	RL	RL	EMBL; AF530559; AAC94404.1; -.	
J. Biol. Chem. 275:36172-36180(2000).	RL	SQ	SEQUENCE 443 AA; 47672 MW;	720BEC4C0718FB14 CRC64;
[2]	RN	Query Match	64.3%; Score 81; DB 11; Length 443;	
SEQUENCE FROM N.A.	RP	Best Local Similarity 75.0%; Pred. No. 0.00051;		
STRAIN=F344;	RC	Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps		
Hu B., Wang X., Wang Y.;	RA			
"Rattus norvegicus cDNA sequence highly expressed in A1-5 cell line	RT			
(identical to osteoregulin).";	RT			
Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.	DR	DR	2 DLQERGNDISPFSGDQPF 21	
EMBL; AF560922; AAC33366.1; -.	DR	DR	173 DLLVRGNDVPFFSGDQHF 192	
EMBL; AF520558; AACM94403.1; -.	DR			
SEQUENCE 435 AA; 46515 MW; D587F82968A26BCB CRC64;	SQ			
RESULT 9				
Q8NC19	AC	SEQUENCE FROM N.A.	PRELIMINARY;	
Q8NC19;	AC	Q8NC19;		
DT	01-OCT-2002	(TREMBLrel. 22; Created)		
01-OCT-2002	DT	01-OCT-2002	(TREMBLrel. 22; Last sequence update)	
01-OCT-2002	DT	01-OCT-2002	(TREMBLrel. 22; Last annotation update)	
Osteoregulin.	DE		Hypothetical protein FLJ9095.	
Homo sapiens (Human).	OS	OS		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	OC		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	OC		
NCBI_TaxID=9606;	RN	RN	[1]	
SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.		
STRAIN=Placenta;	RC	RC		
Izogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,	RA	RA		
RA	RA	RA		
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,	RA	RA		
RA	RA	RA		
Yanamoto J., Wakamatsu A., Nakano Y., Kojima S., Nagahari K.,	RA	RA		
RA	RA	RA		
Masuko Y., Ono T., Okano K., Yoshihikawa Y., Aotsuka S., Sasaki N.,	RA	RA		
RA	RA	RA		
Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;	RA	RA		
RT	RT	RT	"NEMO" human cDNA sequencing project.";	
"NEMO" human cDNA sequencing project.";	RL	RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
AK075076; BAC11386.1; -.	DR	DR		
Hypothetical protein.	RW	RW		
SEQUENCE 275 AA; 31358 MW;	SQ	SQ		
AFOB426A671B665C CRC64;				
Query Match				
Best Local Similarity 93.5%; Score 80; DB 4; Length 275;				
Matches 15; Conservative 15; Mismatches 0; Indels 1; Gaps 0;				
1 DLQERGNDISPFSGDQPF 16	Qy	Qy		
179 DLLVRGNDVPFFSGDQHF 198	Db	Db	242 DLLVRGNDVPFFSGDQHF 257	
RESULT 10				
Q8K416	AC	SEQUENCE FROM N.A.	PRELIMINARY;	
Q8K416;	AC	Q8K416;		
DT	01-OCT-2002	(TREMBLrel. 22; Created)		
01-OCT-2002	DT	01-OCT-2002	(TREMBLrel. 22; Last sequence update)	
01-NR-2003	DT	01-NR-2003	(TREMBLrel. 23; Last annotation update)	
Osteoregulin.	DE			
MEPE	OS			
Mus musculus (Mouse).	OS			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	OC			
NCBI_TaxID=10090;	OX			
SEQUENCE FROM N.A.	RN			
Gowan L.C., Petersen D.N., Vail A.L., Stock J., Tkalcevic G.T.,	RA			
Simmons H.A., Chidsey-Prink K.L., Ke H., McNeish J., Brown T.A.;	RA			
"Targeted disruption of the osteoregulin gene results in increased	RT			
bone density.";	RT			
Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.	RL			
EMBL; AP299661; AACM76871.1; -.	DR			
MGI; MGI:2137314; Mepe.	DR			
SEQUENCE 441 AA; 46872 MW;	SQ	SEQUENCE 441 AA; 46872 MW;	AA1947BF9E2E300 CRC64;	
Query Match				
Best Local Similarity 75.0%; Score 81; DB 11; Length 441;				
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;				
OB1UP7	ID	OB1UP7	PRELIMINARY;	
OB1UP7;	AC	OB1UP7;		
01-MAR-2003	DT	01-MAR-2003	(TREMBLrel. 23; Created)	
01-MAR-2003	DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)	
01-MAR-2003	DT	01-MAR-2003	(TREMBLrel. 23; Last annotation update)	
Similar to phospholipase B.	DE			
RESULT 8				

OS	Homo sapiens (Human)	Chordata; Craniata; Vertebrata; Euteleostomi;	DR	EMBL; AB085239; BAB6823; 1; -.
OC	Eukaryota; Metazoa; Chordata	InterPro; IPR010559; Fmtethyd_synth.	DR	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Pfam; PF01268; PTMFS; 1.	DR	
NCBI_TaxID=9606;		KW Ligase.	KW	
[1]	SEQUENCE FROM N.A.	FT NON_TER	FT	
RP	TISSUE=Brain;	FT NON_TER	FT	
RC	Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.	FT NON_TER	FT	
RA	EMBL; BCO42674; AAH42674; 1; -.	FT NON_TER	FT	
RL	SEQUENCE 423 AA; 47354 MW; A20A193491BA780C CRC64;	FT NON_TER	FT	
SQ	SEQUENCE 423 AA; 47354 MW; A20A193491BA780C CRC64;	FT NON_TER	FT	
Query Match	Score 53; DB 4; Length 423;	Query Match	Score 50; DB 2; Length 356;	
Best Local Similarity	42.1%; Pred. No. 9.4;	Best Local Similarity	42.9%; Pred. No. 22;	
Matches	12; Conservative 2; Mismatches 9; Indels 0; Gaps 0;	Matches	9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;	
Qy	1 TDLOERGNDNDISPPFGDQPFKD 23	Qy	2 DLQERGNDNDISPFSGDGQPK 22	
Db	295 TPINERGDTDLTFFEDCFHFSD 317	Db	80 DLQDRENILGITSDGKPF 100	
RESULT 13		RESULT 13		
	Q8EH99	Q8EH99	PRELIMINARY;	PRT; 1007 AA.
	ID Q8EH99;	ID Q8EH99;	PRELIMINARY;	PRT; 1007 AA.
	AC Q8EH99;	AC Q8EH99;	PRELIMINARY;	PRT; 1007 AA.
	DT 01-MAR-2003 (TREMBLrel. 23, Created)	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
	DE Conserved hypothetical protein.	DE Conserved hypothetical protein.		
	GN SO1309.	GN SO1309.		
	OS Shewanella oneidensis.	OS Shewanella oneidensis.		
	OC Bacterium; Protoobacteria; Gammaproteobacteria; Alteromonadales;	OC Bacterium; Protoobacteria; Gammaproteobacteria; Alteromonadales;		
	OC Alteromonadaceae; Shewanella.	OC Alteromonadaceae; Shewanella.		
	OX NCBI_TaxID=70063;	OX NCBI_TaxID=70063;		
	RN [1]	RN [1]		
	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.		
	RC STRAIN=MR-1;	RC STRAIN=MR-1;		
	RX MEDLINE=22297686; PubMed=12368813;	RX MEDLINE=22297686; PubMed=12368813;		
	RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,	RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,		
	RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methé B., Clayton R.A.,	RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methé B., Clayton R.A.,		
	RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,	RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,		
	RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,	RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,		
	RA Madupu R., Petersen J.D., Umayam L.A., White O., Wolf P.M.,	RA Madupu R., Petersen J.D., Umayam L.A., White O., Wolf P.M.,		
	RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,	RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,		
	RA Mueller J., Khoouri H., Gill J., Utterback T.R., McDonald L.A.,	RA Mueller J., Khoouri H., Gill J., Utterback T.R., McDonald L.A.,		
	RA Feldblyum T.V., Smith H.O., Ventre J.C., Nelson K.H., Fraser C.M.,	RA Feldblyum T.V., Smith H.O., Ventre J.C., Nelson K.H., Fraser C.M.,		
	RT "Genome sequence of the dissimilatory metal ion-reducing bacterium	RT "Genome sequence of the dissimilatory metal ion-reducing bacterium		
	RT Shewanella oneidensis".	RT Shewanella oneidensis".		
	PL Nat. Biotechnol. 20:1118-1123 (2002).	PL Nat. Biotechnol. 20:1118-1123 (2002).		
	DR EMBL; AE015574; AA54374.1; -.	DR EMBL; AE015574; AA54374.1; -.		
	DR TIGR; SO1309; -.	DR TIGR; SO1309; -.		
	KW Hypothetical protein; Complete proteome.	KW Hypothetical protein; Complete proteome.		
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RESULT 14		RESULT 14		
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	ID Q9VYY0;	ID Q9VYY0;	PRELIMINARY;	PRT; 793 AA.
	AC Q9VYY0;	AC Q9VYY0;	PRELIMINARY;	PRT; 793 AA.
	DT 01-MAY-2000 (TREMBLrel. 13, Created)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)		
	DE CG14085 protein.	DE CG14085 protein.		
	GN CG14085.	GN CG14085.		
	OS Drosophila melanogaster (Fruit fly).	OS Drosophila melanogaster (Fruit fly).		
	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
	OC Epioptera; Diptera; Drosophilidae; Drosophila.	OC Epioptera; Diptera; Drosophilidae; Drosophila.		
	NCBI_TaxID=7227;	NCBI_TaxID=7227;		
	OS Drosophila melanogaster (Fruit fly).	OS Drosophila melanogaster (Fruit fly).		
	RA Matsui H., Tajima K., Ogata K.;	RA Matsui H., Tajima K., Ogata K.;		
	RT "Universities of Formyltetrahydrofolate Synthetase Genes Recovered from	RT "Universities of Formyltetrahydrofolate Synthetase Genes Recovered from		
	RT Runmed Contents."	RT Runmed Contents."		
	RA Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.	RA Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.		
	RN NCBI_TaxID=77133;	RN NCBI_TaxID=77133;		
	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.		
	RA Matsui H., Tajima K., Ogata K.;	RA Matsui H., Tajima K., Ogata K.;		
	RT "Universities of Formyltetrahydrofolate Synthetase Genes Recovered from	RT "Universities of Formyltetrahydrofolate Synthetase Genes Recovered from		
	RT Runmed Contents."	RT Runmed Contents."		
	RA Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.	RA Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.		

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RC		KW Hypothetical protein; Complete proteome.
RX	MEDLINE=20196006; PubMed=10731132;	SQ SEQUENCE 326 AA; 34230 MW; 9D5CD723B67DB86 CRC64;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	Query Match 38.3%; Score 49;
RA	Amanatidis P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Best Local Similarity 40.0%; DB 16;
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	Pred. No. 29;
RA	Sutton G.G., Woottman J.R., Yandell M.D., Zhang Q., Chen L.X.,	Matches 10; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D.,	Qy 5 ERGDNDISPFSC-----DQPF 21
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,	RA 163 DSADNPVAPFSSAVDVKLEKRDGQPF 187
RA	Abrial J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beezon K.Y., Benos P.V., Berman B.P., Bhandari D.,	
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottkov S.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Danile C., Daviss P., Dietz S.M.,	Search completed: January 29, 2004, 12:40:18
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	Job time : 34.8947 secs
RA	Dodson K., Doupe L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	
RA	Fobler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RA	Głodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Milashina N.V., Molaro C., Morris J., Moskrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,	
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puris V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	
RT	"The genome sequence of <i>Drosophila melanogaster</i> ,"	
RL	Science 287:2185-2195(2000).	
DR	EMBL; AE003517; AAF49175.1;	
DR	FLYBase; FBgn0036859; CG14085.	
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OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	ID QBNQV1
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RC	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
RA	Nakagawa S.;	DE Hypothetical Protein Cg11322.
RT	"Complete genomic sequence of <i>Corynebacterium glutamicum</i> ATCC 13032."	GN Corynebacterium glutamicum (Brevibacterium flavum).

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Phosphatocan polyp	11	82	100.0	525	22	AAB61689
Human phosphatocan	12	82	100.0	525	23	ABB05226
Human oncogenic o	13	82	100.0	525	23	AAE12227
Human osteoregulin	14	82	100.0	540	22	AAB89923
Human osteoregulin	15	82	100.0	556	22	AAB89921
Dental product bon	16	77	93.9	40	23	AAU93703
Protein of a calcu	17	77	93.9	40	23	AAO2353
Human ODN calcium	18	71	86.6	19	23	AAE12320
Rat osteoregulin	19	71	86.6	435	22	AAB89918
Mouse osteoregulin	20	71	86.6	441	22	AAB89919
Peptide of a calci	21	66	80.5	12	23	AAO2372
Dental product bon	22	60	73.2	15	23	AAU93725
C-terminal amide	23	60	73.2	15	23	AAO23738
Dental Product bon	24	60	73.2	33	23	AAU93710
Peptide of matrix	25	60	73.2	33	23	AAO23360
Human polypeptide,	26	60	73.2	275	22	AAM93507
Dental Product bon	27	55	67.1	15	23	AAU93723
C-terminal amidate	28	55	67.1	15	23	AAO23736
Dental product bon	29	49.5	60.4	40	23	AAU93704
Protein of matrix	30	49.5	60.4	40	23	AAO23354
Dental product bon	31	49	59.8	30	23	AAU93706
Peptide of matrix	32	49	59.8	30	23	AAO23356
Dental Product bon	33	48.5	59.1	35	23	AAU93705
Peptide of matrix	34	48.5	59.1	35	23	AAO23355
Mouse type II integr	35	44.5	54.3	111	22	AAU73963
Drosophila melanog	36	44.5	54.3	793	22	ABB63873
Human polypeptides	37	44	53.7	107	22	AAO12478
Novel human diagno	38	43	52.4	94	22	ABG03384
Propionibacterium	39	43	52.4	648	22	AAU5077
Drosophila melanog	40	42	51.2	1228	22	ABB71296
Human bone marrow	41	50.0	109	22	AAE1214	
Human polypeptide	42	41	50.0	112	22	AAO23626
Human phospholipas	43	41	50.0	472	23	ABP5556
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SUMMARIES						
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2	82	100.0	15	AAU93727	C-terminal amide	XX
3	82	100.0	23	AAU93726	Dental product bon	XX
4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix	DR
7	82	100.0	430	AAV53812	Amino acid sequenc	XX
8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
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4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix	DR
7	82	100.0	430	AAV53812	Amino acid sequenc	XX
8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
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4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix	DR
7	82	100.0	430	AAV53812	Amino acid sequenc	XX
8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
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3	82	100.0	23	AAU93726	Dental product bon	XX
4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix	DR
7	82	100.0	430	AAV53812	Amino acid sequenc	XX
8	100.0	430	22	AAH65622	Truncal product	PT
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4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix	DR
7	82	100.0	430	AAV53812	Amino acid sequenc	XX
8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
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8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
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5	82	100.0	97	AAU93581	Dental product bon	XX
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8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
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8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
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8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	82	100.0	15	AAU93724	Dental product bon	XX
2	82	100.0	15	AAU93727	C-terminal amide	XX
3	82	100.0	23	AAU93726	Dental product bon	XX
4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix	DR
7	82	100.0	430	AAV53812	Amino acid sequenc	XX
8	100.0	430	22	AAH65622	Truncal product	PT
9	82	100.0	509	AAH82922	diseases comprises a base material and a compound comprising specific	PT
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	82	100.0	15	AAU93724	Dental product bon	XX
2	82	100.0	15	AAU93727	C-terminal amide	XX
3	82	100.0	23	AAU93726	Dental product bon	XX
4	82	100.0	23	AAU93725	C-terminal amide	XX
5	82	100.0	97	AAU93581	Dental product bon	XX
6	82	100.0	97	AAU93311	Protein of matrix</td	

PT amino acid in a sequence containing the integrin binding motif -  
 XX Claim 12; Page 21; 44pp; English.

CC The present invention relates to dental products such as toothpastes,  
 CC mouthwash and dental floss comprising a base material and a compound  
 CC which promotes bone growth. Such compounds are peptide sequences  
 CC comprising 10-50 amino acids and containing an integrin binding  
 CC motif such as RGD in the D- or L- form, preferably the L-configuration.  
 CC The peptides of the invention are useful for treating or preventing  
 CC skeletal diseases such as dental disease. The peptides enhance tooth  
 CC and/or alveolar bone growth on areas where deterioration has occurred,  
 CC as well as the growth or recruiting of osteoblast or odontoblast cells  
 CC on the surface of the new skeletal growth. AAU93681-AAU93726 represent  
 CC bone growth enhancing peptides for use in dental products.  
 XX Sequence 15 AA;

Query Match 100.0%; Score 82; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERGDNDISPGDQ 15  
 Db 1 ERGDNDISPGDQ 15

RESULT 2

AAQ20377 standard; peptide; 15 AA.  
 XX AAQ20377;

DT 31-MAY-2002 (first entry)

XX C-terminal amidated synthesised peptide D-00004.

XX Bone growth; RGD motif; integrin binding motif; calcium binding motif;  
 KW Glycosaminoglycan binding motif; bone loss; renal phosphate excretion;  
 KW alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;  
 KW weakness; D00004.

XX Synthetic.

FH Key Location/Qualifiers

FT Modified-site 15  
 FT /note= "C-terminal amide"

XX WO200214360-A1.

XX PD 21-FEB-2002.

XX PF 14-AUG-2001; 2001WO-US25542.

XX PR 16-AUG-2000; 2000US-0641034.

XX PR 19-MAR-2001; 2001US-0812485.

XX DR 2002-291971/33.

XX PA (BIGB-) BIG BEAR BIO INC.

XX PI Yoneda T, Nomizu M, Kumagai Y;

XX PN WO2002-329525/36.

XX DR WPI; 2002-329525/36.

XX PS Claim 7; Page 21; 44pp; English.

XX CC The present invention relates to dental products such as toothpastes,  
 CC mouthwash and dental floss comprising a base material and a compound  
 CC which promotes bone growth. Such compounds are peptide sequences  
 CC comprising 10-50 amino acids and containing an integrin binding  
 CC motif such as RGD in the D- or L- form, preferably the L-configuration.  
 CC The peptides of the invention are useful for treating or preventing  
 CC skeletal diseases such as dental disease. The peptides enhance tooth  
 CC and/or alveolar bone growth on areas where deterioration has occurred,  
 CC as well as the growth or recruiting of osteoblast or odontoblast cells  
 CC on the surface of the new skeletal growth. AAU93681-AAU93726 represent  
 CC bone growth enhancing peptides for use in dental products.

XX SQ Sequence 23 AA;

Query Match 100.0%; Score 82; DB 23; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX PT Example 1; Page 23; 50pp; English.

CC The invention relates to a peptide compound capable of enhancing bone  
 CC growth, and comprising 10-50 amino acids in a sequence, where the amino  
 CC acids are in D- or L- conformation and the sequence comprises a motif  
 CC selected from an integrin binding motif, a glycosaminoglycan binding  
 CC motif and a calcium binding motif. The peptide of the invention is useful  
 CC for reducing bone loss and for reducing renal phosphate excretion in an  
 CC individual. The peptide is useful for promoting regeneration of alveolar  
 CC bone and/or teeth, and increases the number and activity of odontoblasts  
 CC /osteoclasts that help form dental tissues. The peptide is also useful  
 CC for treating or preventing a condition associated with skeletal loss or  
 CC weakness. This sequence represents a C-terminal amidated synthesised  
 peptide D-00004 of the invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 23; Length 23;

Best Local Similarity 100.0%; Pred. No. 6.8e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ERGDNDISPFSGDGQ	15.	AAU93681	AAU93681 standard; protein; 97 AA.
Db	5	ERGDNDISPFSGDGQ	19	XX	
				AC	AAU93681;
				XX	
RESULT 4				DT	02-JUL-2002 (first entry)
AA020379	ID	AA020379 standard; peptide; 23 AA.		DE	Dental product bone growth enhancing peptide #1.
XX	XX			XX	
AA020379;	AC			XX	
XX	XX			XX	
31-MAY-2002	(first entry)			XX	
DT				XX	Dental product; toothpaste; mouthwash; dental floss; bone growth; KW
XX				KW	integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; osteopathic.
DE	C-terminal amidated synthesised peptide D-00006.			XX	
XX				OS	Synthetic.
OS				XX	
XX				PN	WO200213775-A1.
FH	Key	Location/Qualifiers		XX	
FT	Modified-site	23		PD	21-FEB-2002.
FT	/note=	"C-terminal amide"		XX	
XX				PF	09-AUG-2001; 2001WO-US255401.
XX				XX	
XX				PR	16-AUG-2000; 2000US-225879P.
XX				XX	
(BIGB-)	BIG BEAR BIO INC.			PA	
XX				XX	
PI	Yoneida T, Nomizu M, Kumagai Y;			PT	Dental product useful for treating skeletal diseases e.g. dental
XX				PT	diseases comprises a base material and a compound comprising specific
XX				PT	amino acid in a sequence containing the integrin binding motif.
XX				XX	
PS	Disclosure; Page 11; 44pp; English.			DR	
XX				WPI;	2002-329525/36.
XX				XX	
XX				XX	The present invention relates to dental products such as toothpastes,
CC				CC	mouthwash and dental floss comprising a base material and a compound
CC				CC	which promotes bone growth. Such compounds are peptide sequences
CC				CC	comprising 10-50 amino acids and containing an integrin binding
CC				CC	motif such as RGD in the D- or L- form, preferably the L-configuration.
CC				CC	The peptides of the invention are useful for treating or preventing
CC				CC	skeletal diseases such as dental disease. The peptides enhance tooth
CC				CC	and/or alveolar bone growth on areas where deterioration has occurred,
CC				CC	as well as the growth or recruiting of osteoblast or odontoblast cells
CC				CC	on the surface of the new skeletal growth. AU93681-AAU93726 represent
CC				CC	bone growth enhancing peptides for use in dental products.
XX				XX	
SQ	Sequence 97 AA;			PS	
				Query Match	100 0%;
				Best Local Similarity	100 0%;
				Mismatches	0;
				Indels	0;
				Gaps	0;
				DR	
Qy	1 ERGDNDISPFSGDGQ	15		XX	
Db	47 ERGDNDISPFSGDGQ	61		XX	
				XX	31-MAY-2002 (first entry)
RESULT 6				DT	
AA020331	ID	AA020331 standard; protein; 97 AA.		XX	
XX				AC	Protein of matrix extracellular phosphoglycoprotein containing RGD #1.
XX				XX	KW
XX				DE	glycosaminoglycan binding motif; integrin binding motif; calcium binding motif;
XX				KW	alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
XX				KW	weakness; matrix extracellular phosphoglycoprotein.
SQ	Sequence 23 AA;			XX	
				Query Match	100 0%;
				Best Local Similarity	100 0%;
				Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1 ERGDNDISPFSGDGQ	15		XX	
Db	5 ERGDNDISPFSGDGQ	19		XX	
				XX	RESULTS 5



	/note= "Casein kinase II phosphorylation site"	XX	Key Location/Qualifiers
FT	427..430	FT	Misc-difference 161..192
FT	/note= "Casein kinase II phosphorylation site"	XX	/note= "the amino acid residues in this region are indicated incorrectly in the sequence provided in the sequence listing"
PN	W09960017-A2.	PN	WO200132878-A2.
XX	25-NOV-1999.	XX	XX
PD		PD	10-MAY-2001.
XX	18-MAY-1999;	XX	XX
PF	99WO-EP03403.	PF	31-OCT-2000; 2000WO-EPI0747.
XX	18-MAY-1998;	XX	XX
PR	98GB-0010681.	PR	04-NOV-1999; 99US-0434185.
PR	04-SEP-1998;	PR	08-NOV-1999; 99GB-0026424.
XX	98GB-0019387.	XX	XX
PA	(UNLO ) UNIV COLLEGE LONDON.	PA	(UNLO ) UNIV COLLEGE LONDON.
XX		XX	
PA	Rowe P;	PA	Rowe P;
XX		XX	
DR	WPI: 2000-053262/04.	DR	WPI: 2001-343487/36.
N-PSDB;	AZ36447.	N-PSDB;	AAF83159.
XX		XX	
PT	New polypeptides involved in the regulation of phosphate metabolism	PT	New phosphatonin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, skeletal formation e.g. osteoporosis, Page's disease, gout -
PT	useful for diagnosing and treating disorders related to phosphate metabolism -	PT	
PS	Claim 6; Fig 8; 136pp; English.	PS	Claim 4; Fig 8; 135pp; English.
XX		XX	
CC	The present sequence represents a phosphatonin polypeptide (also called Metatatic-tumour Excreted Phosphaturic-Element (MEPE)). The level of phosphatonin in a subject modulates Na <sup>+</sup> -dependent phosphate cotransport, vitamin D metabolism and/or bone mineralisation. The phosphatonin polypeptides, polynucleotides, vectors and antibodies are used to treat phosphate metabolism related disease. They are used for treatment of hyperphosphataemia, or renal osteodystrophy, hyperparathyroidism in renal dialysis/pre-dialysis, secondary hyperparathyroidism or osteitis fibrosa cystica, or X-linked hypophosphataemic rickets, hereditary hypophosphataemic rickets with hypocalciuria (HHRH), hypomineralised bone lesions, stunted growth in juveniles, oncogenic hypophosphataemic osteomalacia, renal phosphate leakage, renal osteodystrophy, osteoporoisis, vitamin D resistant rickets, osteoporosis, vitamin D resistant rickets, and organ resistance, renal Fanconi syndrome, autosomal rickets, Paget's disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide may also be used to manufacture combined preparations for simultaneous, separate or sequential use for the treatment of phosphate metabolism disorders. A transformed osteoblast or bone cell line capable of phosphatonin overexpression is useful for the production of phosphatonin.	CC	The invention relates to a novel human protein, metatatic-tumour excreted phosphaturic element (MEPE) or phosphatonin (modulator of phosphate and vitamin-D metabolism). The phosphatonin polypeptides, polynucleotides and specific antibodies are useful for treating a disorder of phosphate or vitamin D metabolism, skeletal formation and mineralization. Phosphatonins are used to treat hyperphosphataemia, renal osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica or gout. It is used to prepare a medicament for treating X-linked hypophosphataemic rickets, hereditary hypophosphataemic rickets with hypocalciuria (HHRH), hypomineralised bone lesions, stunted growth in juveniles, oncogenic hypophosphataemic osteomalacia, renal phosphate leakage, renal osteodystrophy, osteoporoisis, vitamin-D resistant rickets, end organ resistance, renal Fanconi syndrome, autosomal rickets, CC disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. Phosphatonin polynucleotides are useful as molecular weight markers on Southern Gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatonin polypeptides are also useful for identifying agonists and antagonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents a truncated form of phosphatonin (MEPE).
CC		CC	
CC	Sequence 430 AA;	CC	Query Match 100.0%; Score 82; DB 22; Length 430;
CC	Best Local Similarity 100.0%; Pred. No. 2e-05;	CC	Best Local Similarity 100.0%; Pred. No. 2e-05;
CC	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ	AAAB62669	SQ	Query 1 ERGDNDISPFSGDQ 15
Db	AAAB62669 standard; Protein; 430 AA.	Db	151 ERGDNDISPFSGDQ 165
RESULT 8		RESULT 9	
ID AAB62669		ID AAB82922	
XX		XX	
XX	23-JUL-2001 (first entry)	XX	AAB82922 standard; Protein; 509 AA.
AC		AC	
XX		XX	
DE		DE	
XX		XX	
DT		DT	21-DEC-2001 (first entry)
XX		XX	Human osteoregulin (mature polypeptide).
DE			Osteoregulin; human; bone; homeostasis; adipose; calcification;
XX			KW
OS			Homo sapiens.

KW atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;  
therapy.

XX Homo sapiens.

OS Homo sapiens.

NN EP1130098-A2.

XX PD 05-SEP-2001.

XX PF 27-FEB-2001; 2001EP-0301768.

XX PR 29-FEB-2000; 2000US-185617P.

XX PR 22-SEP-2000; 2000US-234500P.

XX PA (PFIZ ) PFIZER PROD INC.

XX Brown TA, De Wet JR, Gowen LC, Hames LM;

XX WPI: 2001-604111/69.

DR N-PSDB; AAH26810.

XX Novel osteoregulin polypeptide useful for regulating bone homeostasis,

PT adiposity and calcification of atherosclerotic plaques comprises

PT measuring the activity of osteoregulin -

XX Claim 1; Page 54-55; 90pp; English.

CC The present sequence is that of human osteoregulin, a novel mature

CC polypeptide, i.e. lacking an N-terminal signal sequence.

CC Osteoregulin is a novel protein which plays a role in regulating

CC bone homeostasis, adiposity, and the calcification of

CC atherosclerotic plaques. 2 Splice variants of human osteoregulin

CC were identified (see also AAB82923). The invention provides novel

CC osteoregulin proteins nucleic acids which encode them, vectors,

CC antibodies, host cells which express heterologous osteoregulins, and

CC animal cells and mammals with a targeted disruption of an

CC osteoregulin gene. The invention also provides screening assays

CC to identify modulators of osteoregulin activity as well as methods

CC of treating mammals for diseases or disorders associated with

CC osteoregulin activity. The modulators of activity may be useful

CC in the manufacture of a medicament for, as well as for treating, a

CC mammal in need of regulation of bone mass and/or density, adiposity,

CC vascular flexibility, and/or atherosclerotic plaque calcification

CC (claimed), for treating and preventing osteoporosis, and for

CC stimulating bone repair and regeneration.

XX Sequence 509 AA;

CC Query Match 100.0%; Score 82; DB 22;

CC Best Local Similarity 100.0%; Pred. No. 2.4e-05;

CC Matches 15; Conservative 0; Mismatches 0;

CC Indels 0; Gaps 0;

CC OS

XX Query Match 100.0%; Score 82; DB 22;

XX Best Local Similarity 100.0%; Pred. No. 2.5e-05;

XX Matches 15; Conservative 0; Mismatches 0;

XX Indels 0; Gaps 0;

XX OS

PH Key Peptide Location/Qualifiers  
FT FT 1..37  
FT FT /label= Signal\_Peptide  
FT FT 38..525  
XX PN EP1130098-A2.  
XX PN EP1130098-A2.

PD 05-SEP-2001.  
XX PD 05-SEP-2001.

XX PF 27-FEB-2001; 2001EP-0301768.

XX PR 29-FEB-2000; 2000US-185617P.

PR 22-SEP-2000; 2000US-234500P.

XX PR 22-SEP-2000; 2000US-234500P.

XX PA (PFIZ ) PFIZER PROD INC.

XX PI Brown TA, De Wet JR, Gowen LC, Hames LM;

XX XX DR WPI; 2001-604111/69.

DR N-PSDB; AAH26810.

XX PS Claim 1; Page 45-47; 90pp; English.

XX CC The present sequence is that of human osteoregulin, a novel protein

CC which plays a role in regulating bone homeostasis, adiposity, and

CC the calcification of atherosclerotic plaques. The sequence is

CC predicted from the nucleotide sequence (see AAH26808) of isolated

CC osteoblast cDNA. A splice variant of human osteoregulin was also

CC identified (see AAB82921). The invention provides novel

CC osteoregulin proteins, nucleic acids which encode them, vectors,

CC antibodies, host cells which express heterologous osteoregulins, and

CC animal cells and mammals with a targeted disruption of an

CC osteoregulin gene. The invention also provides screening assays

CC to identify modulators of osteoregulin activity as well as methods

CC of treating mammals for diseases or disorders associated with

CC osteoregulin activity. The modulators of activity may be useful

CC in the manufacture of a medicament for, as well as for treating, a

CC mammal in need of regulation of bone mass and/or density, adiposity,

CC vascular flexibility, and/or atherosclerotic plaque calcification

CC (claimed), for treating and preventing osteoporosis, and for

CC stimulating bone repair and regeneration.

XX SQ Sequence 525 AA;

CC Query Match 100.0%; Score 82; DB 22;

CC Best Local Similarity 100.0%; Pred. No. 2.5e-05;

CC Matches 15; Conservative 0; Mismatches 0;

CC Indels 0; Gaps 0;

CC OS

RESULT 10

ID AAB82920 standard; Protein; 525 AA.

XX AC AAB82920;

XX DT 21-DEC-2001 (first entry)

DE Human osteoregulin.

XX KW Osteoregulin; human; bone; homeostasis; adipose; calcification;

KW atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;

KW therapy.

XX OS Homo sapiens.

PH Key Peptide Location/Qualifiers  
FT FT 1..37  
FT FT /label= Signal\_Peptide  
FT FT 38..525  
XX PN EP1130098-A2.

XX PD 05-SEP-2001.

XX PF 27-FEB-2001; 2001EP-0301768.

XX PR 29-FEB-2000; 2000US-185617P.

PR 22-SEP-2000; 2000US-234500P.

XX PA (PFIZ ) PFIZER PROD INC.

XX PI Brown TA, De Wet JR, Gowen LC, Hames LM;

XX XX DR WPI; 2001-604111/69.

DR N-PSDB; AAH26810.

XX PS Claim 1; Page 45-47; 90pp; English.

XX CC The present sequence is that of human osteoregulin, a novel protein

CC which plays a role in regulating bone homeostasis, adiposity, and

CC the calcification of atherosclerotic plaques. The sequence is

CC predicted from the nucleotide sequence (see AAH26808) of isolated

CC osteoblast cDNA. A splice variant of human osteoregulin was also

CC identified (see AAB82921). The invention provides novel

CC osteoregulin proteins, nucleic acids which encode them, vectors,

CC antibodies, host cells which express heterologous osteoregulins, and

CC animal cells and mammals with a targeted disruption of an

CC osteoregulin gene. The invention also provides screening assays

CC to identify modulators of osteoregulin activity as well as methods

CC of treating mammals for diseases or disorders associated with

CC osteoregulin activity. The modulators of activity may be useful

CC in the manufacture of a medicament for, as well as for treating, a

CC mammal in need of regulation of bone mass and/or density, adiposity,

CC vascular flexibility, and/or atherosclerotic plaque calcification

CC (claimed), for treating and preventing osteoporosis, and for

CC stimulating bone repair and regeneration.

XX SQ Sequence 525 AA;

CC Query Match 100.0%; Score 82; DB 22;

CC Best Local Similarity 100.0%; Pred. No. 2.5e-05;

CC Matches 15; Conservative 0; Mismatches 0;

CC Indels 0; Gaps 0;

CC OS

XX SQ Sequence 525 AA;

CC Query Match 100.0%; Score 82; DB 22;

CC Best Local Similarity 100.0%; Pred. No. 2.5e-05;

CC Matches 15; Conservative 0; Mismatches 0;

CC Indels 0; Gaps 0;

CC OS

RESULT 11

ID AAB62689 standard; Protein; 525 AA.

XX AC AAB62689;

XX DT 23-JUL-2001 (first entry)

DE Phosphatoin polypeptide (MEPE).

XX KW Metastatic-tumour excreted phosphaturic element; MEPE; phosphatoin;

KW phosphate; vitamin-D; skeletal formation; mineralization; truncated;

KW osteopathic; anticout; cytostatic; human.

XX OS Homo sapiens.

XX WO200132878-A2.  
 XX PD 27-DEC-2001.  
 XX PF 20-JUN-2001; 2001WO-JP05263.  
 XX PR XX  
 XX 31-OCT-2000; 2000WO-BP10747.  
 XX PR 21-JUN-2000; 2000JP-0191088.  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX PI Kurokawa T, Yamada T, Morimoto S;  
 XX DR WPI; 2002-139791/18.  
 XX DR N-PSDB; ABA99159, ABA99160.  
 XX PT Phosphatonin of human origin and DNA encoding it for diagnosis and  
 treatment of diseases associated with disorders of phosphate  
 metabolism, e.g., hyperphosphoæmia, arteriosclerosis, heart failure,  
 diabetic renal disease and kidney failure -  
 XX PS Claim 1; Fig 1-4; 130pp; Japanese.  
 XX DR WPI; 2001-343487/36.  
 XX DR N-PSDB; AAF33764.  
 XX PT New phosphatonin polypeptide a regulator of phosphate metabolism, for  
 diagnosing and treating disorders of phosphate, vitamin-D metabolism,  
 skeletal formation e.g. osteoporosis, Paget's disease, gout -  
 XX PS Claim 4; Page 133-134; 135pp; English.  
 XX The invention relates to a novel human protein, metastatic-tumour  
 excreted phosphaturic element (MEPE) or phosphatonin (modulator of  
 phosphate and vitamin-D metabolism). The phosphatonin polypeptides,  
 nucleotides and specific antibodies are useful for treating a  
 disorder of phosphate or vitamin D metabolism, skeletal formation and  
 osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica  
 or gout. It is used to prepare a medicament for treating X-linked  
 hypophosphatemic rickets, hereditary hypophosphatemic rickets with  
 hypercalcuria (HHRH), hypomineralized bone lesions, stunted growth in  
 juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphate  
 leakage, renal osteodystrophy, osteoporosis, vitamin-D resistant rickets,  
 end organ resistance, renal Fanconi syndrome, autosomal rickets, Paget's  
 disease, kidney failure, renal tubular acidosis, cystic fibrosis or  
 sprue. Phosphatonin polynucleotides are useful as molecular weight  
 markers on Southern gels, as diagnostic probes for detecting the presence  
 of a specific mRNA. Phosphatonin polypeptides are also useful for  
 identifying agonists and antagonists, compounds which bind to  
 phosphatonin and drug candidates for therapy of phosphate metabolism  
 disorders. The present sequence represents the amino acid sequence of  
 the entire phosphatonin (MEPE).  
 XX SQ Sequence 525 AA;  
 XX Query Match 100.0%; Score 82; DB 22; Length 525;  
 XX Best Local Similarity 100.0%; Pred. No. 2.5e-05; Indels 0; Gaps 0;  
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX DT 12-FEB-2002 (First entry)  
 XX ID AAE13227 standard; Protein; 525 AA.  
 XX AC AAE13227;  
 XX DE Human oncogenic osteomalacia-related protein-1. (OOM-1).  
 XX KW Human; oncogenic osteomalacia-related protein 1; OOM1; gene therapy;  
 XX KW phosphate homeostasis-related disease; rickets; osteomalacia; cardiot;
 XX KW rhabdomyolysis; cardiopathy; tumour calcinosis; renal failure;  
 XX KW bone mineralisation; phosphaturia; cellular process.  
 XX OS Homo sapiens.  
 XX Key Peptide 1..16  
 XX FT Peptide /label= Signal\_peptide  
 XX FT Protein 17..325  
 /note= "Mature oncogenic osteomalacia-related protein-1  
 (OOM-1)"  
 XX FT Domain 130..142  
 /note= "Calcium binding motif"  
 XX FT Domain 235..258  
 /note= "Calcium binding motif"  
 XX FT Region 247..249

RESULT 12  
 ABB08526 Human phosphatonin.  
 ID ABB08526 standard, protein; 525 AA.  
 XX AC ABB08526;  
 XX DT 23-MAY-2002 (First entry)  
 XX DE Human phosphatonin.  
 XX KW Human phosphatonin; cytosolic; antidiabetic; antiinflammatory;  
 KW hyperphosphoæmia; arteriosclerosis; heart failure;  
 KW diabetic renal disease; kidney failure; cystic fibrosis.  
 XX OS Homo sapiens.  
 PN WO200198495-A1.

RESULT 13  
 AAE13227 Human phosphatonin-1. (OOM-1).  
 ID AAE13227 standard; Protein; 525 AA.  
 XX AC AAE13227;  
 XX DE Human oncogenic osteomalacia-related protein-1. (OOM-1).  
 XX KW Human; oncogenic osteomalacia-related protein 1; OOM1; gene therapy;  
 KW phosphate homeostasis-related disease; rickets; osteomalacia; cardiot;
 KW rhabdomyolysis; cardiopathy; tumour calcinosis; renal failure;  
 KW bone mineralisation; phosphaturia; cellular process.  
 XX OS Homo sapiens.  
 XX Key Peptide 1..16  
 XX FT Peptide /label= Signal\_peptide  
 XX FT Protein 17..325  
 /note= "Mature oncogenic osteomalacia-related protein-1  
 (OOM-1)"  
 XX FT Domain 130..142  
 /note= "Calcium binding motif"  
 XX FT Domain 235..258  
 /note= "Calcium binding motif"  
 XX FT Region 247..249



XX Human osteoregulin.  
 XX  
 KW Osteoregulin; human; bone; homeostasis; adipose; calcification;  
 KW atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 PH 1..37  
 PT /label= Signal\_peptide  
 PT 38..556  
 PT /label= Mature\_protein  
 PT Misc-difference 57  
 PT /note= "encoded by 'TCA'"  
 XX EP1130098-A2.  
 PN PD-2001.  
 XX PD-SEP-2001.  
 XX PF 27-FEB-2001; 2001EP-0301768.  
 XX PR 29-FEB-2000; 2000US-185617P.  
 XX PR 22-SEP-2000; 2000US-234500P.  
 XX PA (PFIZER ) PFIZER PROD INC.  
 DR WPI; 2001-604111/69.  
 DR N-PADB; AAH26809.  
 XX  
 PI Brown TA,  
 XX De Wet JR,  
 PT Gowen LC,  
 PT Hames LM;  
 XX  
 DR  
 PS Claim 1; Page 48-49; 90pp; English.  
 XX  
 CC The present sequence is that of human osteoregulin, a novel protein  
 CC which plays a role in regulating bone homeostasis, adiposity, and  
 CC the calcification of atherosclerotic plaques. The sequence is  
 CC predicted from the nucleotide sequence (see AAH26809) of isolated  
 CC osteoblast cDNA. A splice variant of human osteoregulin was also  
 CC identified (see ARB82920). The invention provides novel  
 CC osteoregulin proteins, nucleic acids which encode them, vectors,  
 CC antibodies, host cells which express heterologous osteoregulins, and  
 CC animal cells and mammals with a targeted disruption of an  
 CC osteoregulin gene. The invention also provides screening assays  
 CC to identify modulators of osteoregulin activity as well as methods  
 CC of treating mammals for diseases or disorders associated with  
 CC osteoregulin activity. The modulators of activity may be useful  
 CC in the manufacture of a medicament for, as well as for treating, a  
 CC mammal in need of regulation of bone mass and/or density, adiposity,  
 CC vascular flexibility, and/or atherosclerotic plaque calcification  
 CC (claimed), for treating and preventing osteoporosis, and for  
 CC stimulating bone repair and regeneration.  
 XX Sequence 556 AA;  
 SQ Score 82; DB 22; Length 556;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ERGDNDISFSFGDQ 15  
 Db 277 ERGDNDISFSFGDQ 291.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 29, 2004, 12:37:19 ; Search time 11.4474 Seconds  
(without alignments)

55.442 Million cell updates/sec

Title: US-09-812-485A-47  
Perfect score: 82  
Sequence: 1 ERGDNDISPFSGDQQ 15

Scoring table: BLOSUM62  
Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cgm2\_6/ptodata/1/iaa/5A COMB .pep: \*  
 2: /cgm2\_6/ptodata/1/iaa/5B COMB .pep: \*  
 3: /cgm2\_6/ptodata/1/iaa/6A COMB .pep: \*  
 4: /cgm2\_6/ptodata/1/iaa/6B COMB .pep: \*  
 5: /cgm2\_6/ptodata/1/iaa/PCTUS COMB .pep: \*  
 6: /cgm2\_6/ptodata/1/iaa/backfile1 .pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	50.0	2039	4 US-09-077-098A-7	Sequence 7, Appli
2	41	50.0	2042	4 US-09-077-098A-6	Sequence 6, Appli
3	40	48.8	302	4 US-09-232-991A-21875	Sequence 21875, A
4	40	48.8	795	3 US-09-370-807-6	Sequence 6, Appli
5	40	48.8	795	4 US-09-921-259-6	Sequence 6, Appli
6	39	47.6	101	4 US-09-232-991A-22399	Sequence 22399, A
7	39	47.6	425	4 US-09-232-991A-31834	Sequence 31834, A
8	38.5	47.0	469	3 US-08-704-711A-16	Sequence 12, Appli
9	38.5	47.0	469	3 US-08-448-489-12	Sequence 12, Appli
10	38.5	47.0	469	4 US-09-521-220-16	Sequence 16, Appli
11	38.5	47.0	469	4 US-09-331-104-23	Sequence 23, Appli
12	38	46.3	169	4 US-09-232-991A-26193	Sequence 26193, A
13	38	46.3	186	4 US-09-328-352-7703	Sequence 7703, Ap
14	38	46.3	3038	1 US-08-450-332-2	Sequence 2, Appli
15	38	46.3	3038	2 US-08-631-640-2	Sequence 2, Appli
16	38	46.3	3038	3 US-09-004-400C-2	Sequence 2, Appli
17	37	45.1	232	4 US-09-134-001C-5220	Sequence 5220, Ap
18	37	45.1	245	4 US-09-232-991A-30321	Sequence 30321, A
19	37	45.1	256	5 PCT-US95-01314-55	Sequence 55, Appli
20	37	45.1	301	2 US-08-355-844-2	Sequence 2, Appli
21	37	45.1	301	5 PCT-US95-16126-2	Sequence 23810, A
22	37	45.1	313	4 US-09-252-991A-239810	Sequence 31126, A
23	37	45.1	317	4 US-09-25-991A-31126	Sequence 1, Appli
24	37	45.1	394	1 US-07-637-870-1	Sequence 1, Appli
25	37	45.1	394	1 US-07-637-399-1	Sequence 5, Appli
26	37	45.1	394	1 US-07-640-476-5	Sequence 1, Appli
27	37	45.1	394	1 US-08-112-703-1	Sequence 1, Appli

RESULT 1  
US-09-077-098A-7

; Sequence 7, Application US/09077098A  
; Patent No. 6544519

## GENERAL INFORMATION:

APPLICANT: TOKUNAGA, Eiji  
MATSUO, Kazuo  
HAMADA, Fukubaburo  
TOKIYOSHI, Sachio

TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWNY AND NEIMARK  
STREET: 624 Ninth Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/077, 098A  
FILING DATE: 19-May-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP97/03222  
FILING DATE: 12-SEP-1997  
APPLICATION NUMBER: JP 27,148/1996  
FILING DATE: 19-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: KORNBAU, Anne M.  
REGISTRATION NUMBER: 25, 618  
REFERENCE/DOCKET NUMBER: TOKUNAGA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-26-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2039 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-077-098A-7

## ALIGNMENTS

Query Match 50.0%; Score 41; DB 4; Length 2039;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+02; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 0;

Qy 4 DNDISPFSGD 13  
 Db 1591 DGDISPTSGD 1608

RESULT 2  
 US-09-077-098A-6  
 ; Sequence 6, Application US/09077098A  
 ; Patent No. 6544519  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TOKUNAGA, Eiji  
 ; SAKAGUCHI, Masashi  
 ; MATSUO, Kazuo  
 ; HAMADA, Fukusaburo  
 ; TOKIYOSHI, Sachio  
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS  
 ; PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NETMARK  
 ; STREET: 624 Ninth Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/077,098A  
 ; FILING DATE: 19-May-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/JP97/03222  
 ; FILING DATE: 12-SEP-1997  
 ; APPLICATION NUMBER: JP 27,148/1996  
 ; FILING DATE: 19-SEP-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KORNBAU, Anne M.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: TOKUNAGA-1  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2042 amino acids  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 ; US-09-077-098A-6

Query Match 50.0%; Score 41; DB 4; Length 2042;  
 Best Local Similarity 80.0%; Pred. No. 4.1e+02; Indels 2; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 2;

Qy 4 DNDISPFSGD 13  
 Db 1591 DGDISPTSGD 1608

RESULT 3  
 US-09-232-999A-21875  
 ; Sequence 2875, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.1.6  
 ; CURRENT APPLICATION NUMBER: US/09/252,391A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO: 21875  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-21875

Query Match 48.8%; Score 40; DB 4; Length 302;  
 Best Local Similarity 46.7%; Pred. No. 76;  
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ERGNDIDSPFSGCQ 15  
 Db 137 QRGDIDVAILFGGCR 151

RESULT 4  
 US-09-370-807-6  
 ; Sequence 6, Application US/09370807  
 ; Patent No. 6297034  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cahoon, Rebecca E.  
 ; APPLICANT: Falco, S. Carl  
 ; APPLICANT: Rafalski, J. Antoni  
 ; APPLICANT: Sakai, Hajime  
 ; TITLE OF INVENTION: N-End Rule Pathway Enzymes  
 ; FILE REFERENCE: BB-1199  
 ; CURRENT APPLICATION NUMBER: US/09/370,807  
 ; CURRENT FILING DATE: 1999-08-09  
 ; EARLIER APPLICATION NUMBER: 60/096,225  
 ; EARLIER FILING DATE: August 12, 1998  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO: 6  
 ; LENGTH: 795  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; US-09-370-807-6

Query Match 48.8%; Score 40; DB 3; Length 795;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GDNIDISPFG 12  
 Db 427 GDRELNPFG 436

RESULT 5  
 US-09-321-259-6  
 ; Sequence 6, Application US/09921259  
 ; Patent No. 646534  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cahoon, Rebecca E.  
 ; APPLICANT: Falco, S. Carl  
 ; APPLICANT: Rafalski, J. Antoni  
 ; APPLICANT: Sakai, Hajime  
 ; TITLE OF INVENTION: N-End Rule Pathway Enzymes  
 ; FILE REFERENCE: BB-1199  
 ; CURRENT APPLICATION NUMBER: US/09/921,259  
 ; CURRENT FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: 60/096,225  
 ; PRIOR FILING DATE: August 12, 1998

NUMBER OF SEQ ID NOS: 16  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO 6  
 LENGTH: 795  
 TYPE: PRT  
 ORGANISM: Zea mays  
 US-09-921-259-6

Query Match Score 40.; DB 4; Length 795;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GNDNIDSPFG 12  
 Db 427 GDRELNPFG 436

RESULT 6  
 Sequence 22899, Application US/09252991A  
 Patent No. 6551195

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196\_136  
 CURRENT APPLICATION NUMBER: US/09/252, 991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074, 788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094, 190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 22899  
 LENGTH: 101  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-22899

Query Match Score 39.; DB 4; Length 101;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DNDISPPFSD 13  
 Db 17 DGELKPFSSD 26

RESULT 7  
 Sequence 31834, Application US/09252991A  
 Patent No. 6551195

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196\_136  
 CURRENT APPLICATION NUMBER: US/09/252, 991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074, 788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094, 190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 31834  
 LENGTH: 425  
 TYPE: PRT  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-31834

Query Match Score 39.; DB 4; Length 425;  
 Best Local Similarity 53.3%; Pred. No. 1.6e+02;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ERGDNDISPPFSDGQ 15  
 Db 65 EGGRNDAESTGGQ 79

RESULT 8  
 Sequence 16, Application US/08704711A  
 Patent No. 6114159

GENERAL INFORMATION:  
 APPLICANT: HINZNANN, Bernd  
 TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX METALLOPROTEASES, THEIR PRODUCTION AND USE  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/704, 711A  
 FILING DATE: 20-NOV-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/DE95/00357  
 FILING DATE: 17-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 4438838.1  
 FILING DATE: 21-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 4409663.1  
 FILING DATE: 17-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GRANADOS, Patricia D.  
 REGISTRATION NUMBER: 33,683  
 REFERENCE/DOCKET NUMBER: 26083/124  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEX: (202) 672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 469 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-704-711A-16

Query Match Score 38.5%; DB 3; Length 469;  
 Best Local Similarity 64.3%; Pred. No. 2.1e+02;  
 Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 2 RGDN-DISPPFSDG 14  
 Db 165 RGDDRNNSPFDGFG 178

RESULT 9  
 Sequence 12, Application US/08448489  
 Patent No. 6184022

GENERAL INFORMATION:  
 APPLICANT: SEIKI, Motoharu  
 APPLICANT: SATO, Hiroshi

APPLICANT: SHINAGAWA, Akira  
 TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
 FILE REFERENCE: 55-290P  
 CURRENT APPLICATION NUMBER: US/08/448,489  
 CURRENT FILING DATE: 1995-06-07  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 12  
 LENGTH: 469

TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism: Known Member of Family  
 OTHER INFORMATION: Matrix Metalloproteinase Family  
 IS-08-448-489-12

Query Match	47.0%	Score 38 5;	DB 3;	Length 469;
Best Local Similarity	64.3%;	Pred. No. 2	.1e+02;	
Matches 9;	Conservative	1;	Mismatches 3;	Indels 1;
				Gap

Y	2 RCDN-DISPFSGDG 14			
b	:			
b	165 RGDHRDNSPFDGPG 178			

SEQUENCE RESULT 10  
 IS-09-521-220-16  
 Sequence 16, Application US/09521220  
 Patent No. 6399348

GENERAL INFORMATION:  
 APPLICANT: WILL, Horst  
 HINZMANN, Bernd  
 TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX METALLOPROTEASES, THEIR PRODUCTION AND USE  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/521,220  
 FILING DATE: 08-Mar-2000  
 CLASSIFICATION: <Unknown>  
 21-OCT-1994  
 17-MAR-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/704,711  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: DE 4438838.1  
 FILING DATE: 21-OCT-1994  
 APPLICATION NUMBER: DE 4409653.1  
 FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:  
 NAME: GRANADOS, Patricia D.  
 REGISTRATION NUMBER: 33 683  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5300  
 TELEX: 904136

INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 469 amino acids  
 SPANDEXNESS: single  
 TYPE: amino acid

Qy 3 GNDISPFGDG 14 ; STRANDEDNESS: single  
 Db 6 GGS DISPAG 17 ; TOPOLOGY: linear  
     ; MOLECULE TYPE: protein  
     ; HYPOTHETICAL: YES  
     ; ORIGINAL SOURCE:  
     ; ORGANISM: TPKS Protein  
 US-08-450-332-2

RESULT 13  
 US-09-328-352-7703 ; Sequence 7703, Application US/09328352  
 ; Patent No. 6562558  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: GTC9-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; CURRENT FILING DATE: 1999-06-04  
 ; SEQ ID NO 7703  
 ; LENGTH: 186  
 ; TYPE: PRF  
 ; ORGANISM: Acinetobacter baumannii

US-09-328-352-7703 ; Query Match 46.3%; Score 38; DB 4; Length 186;  
     ; Best Local Similarity 63.6%; Pred. No. 1.9e+03;  
     ; Matches 7; Mismatches 1; Indels 3; Gaps 0;  
 Qy 3 GNDISPFGS 11 ; Query Match 46.3%; Score 38; DB 1; Length 3038;  
     ; Best Local Similarity 63.6%; Pred. No. 1.9e+03;  
     ; Matches 7; Mismatches 1; Indels 3; Gaps 0;  
 Db 77 GETDISPFS 85 ; Query Match 46.3%; Score 38; DB 2; Length 3038;  
     ; Best Local Similarity 63.6%; Pred. No. 1.9e+03;  
     ; Matches 7; Mismatches 1; Indels 3; Gaps 0;

RESULT 14  
 US-08-450-332-2 ; Sequence 2, Application US/08450332  
 ; Patent No. 574450  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VINCI, VICTOR A.  
 ; APPLICANT: CONDER, MICHAEL J.  
 ; APPLICANT: MCADA, PHYLLIS C.  
 ; APPLICANT: REEVES, CHRISTOPHER D.  
 ; APPLICANT: DAVIS, CHARLES R.  
 ; APPLICANT: HENDRICKSON, LEE E.  
 ; APPLICANT: RAMBOSEK, JOHN  
 ; TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE  
 ; NUMBER OF SEQUENCES: 3  
 ; CURRENT APPLICATION DATA:  
 ; ADDRESSSEE: CHRISTINE E. CARTY  
 ; STREET: 126 E. LINCOLN AVENUE, P.O. Box 2000  
 ; CITY: RAHWAY  
 ; STATE: NJ  
 ; ZIP: 07065-0907  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/637,640  
 ; FILING DATE: 23-AUG-1996  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/148,132  
 ; FILING DATE: 01-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: CARTY, CHRISTINE E.  
 ; REGISTRATION NUMBER: 36,099  
 ; REFERENCE/DOCKET NUMBER: 19076  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 908-594-6734  
 ; FAX: 908-594-4720  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3038 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: YES  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: TPKS Protein  
 US-08-637-640-2

Query Match 46.3%; Score 38; DB 2; Length 3038;  
 ; Best Local Similarity 63.6%; Pred. No. 1.9e+03;  
 ; Matches 7; Mismatches 1; Indels 3; Gaps 0;

Qy 1 ERGDNDTSPPFS 11  
Db | | | ; |  
878 ERGKNDDSFPS 888

Search completed: January 29, 2004, 12:41:37  
Job time : 12.4474 secs